

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 30, 2002, 14:59:19 : Search time 41.9 Seconds

(without alignments)
3719.249 Million cell updates/sec

Title: US-09-830-338-1

Perfect score: 7308
Sequence: 1 MATQKASDRISQFDHNL.....SKYLIQKMLPSPRIQK 1403

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A-Geneseq_032802:*

1:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT:*
2:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:*
3:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:*
4:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT:*
5:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT:*
6:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT:*
7:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT:*
8:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT:*
9:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT:*
10:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT:*
11:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT:*
12:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT:*
13:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT:*
14:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT:*
15:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT:*
16:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT:*
17:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT:*
18:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT:*
19:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:*
20:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT:*
21:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:*
22:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7308	100.0	1403	18 AAM20032	Neuronal apoptosis
2	7308	100.0	1403	20 AAY14079	Gonadotropic hormo
3	7308	100.0	1403	21 AAY09539	Human apoptosis in
4	7308	100.0	1403	20 AAY08053	Human NAIP protein
5	7284	99.7	1403	18 AAM20033	Neuronal apoptosis
6	6691	91.6	1295	20 AAY14080	Gonadotropic hormo
7	6691	91.6	1295	20 AAY09540	Human apoptosis in
8	6373.5	87.2	1232	17 AAR98217	Human caspase recr
9	661	9.0	1204	22 AAU02881	Human caspase recr
10	654	8.9	1070	22 AAG67527	Amino acid sequenc
11	653	8.9	1024	22 AAU02880	Human caspase recr

12	566	7.7	841	22 AAM23595	Murine EST encoded
13	545.5	7.5	118	21 AAB35493	Human colon cancer
14	536.5	7.3	738	22 AAG67526	Amino acid sequenc
15	462	6.3	618	18 AAM19746	Human inhibitor of
16	462	6.3	618	18 AAM19583	Human apoptosis in
17	462	6.3	618	18 AAM13545	Human c-IAP1. Hom
18	462	6.3	618	19 AAM69296	Human H1AP-2 prote
19	462	6.3	618	20 AAY33998	Human cellular inh
20	457.5	6.3	612	18 AAM13555	Murine c-IAP. Mus
21	457.5	6.3	612	19 AAM69299	Murine H1AP-2 prot
22	441.5	6.0	591	18 AAM19586	Mouse apoptosis in
23	440	6.0	600	19 AAM69298	Murine H1AP-1 prot
24	437.5	6.0	496	18 AAM19584	Mouse apoptosis in
25	437.5	6.0	496	19 AAM69297	Murine XIAP protei
26	436.5	6.0	604	18 AAM19747	Human inhibitor of
27	436.5	6.0	604	18 AAM13546	Human c-IAP2. Hom
28	436.5	6.0	604	20 AAY52703	Human cellular inh
29	436.5	6.0	604	20 AAY33997	Human cellular inh
30	435	6.0	1141	22 AAB50694	Human API2-MUT chl
31	431.5	5.9	496	18 AAM19745	Mouse inhibitor of
32	431.5	5.9	604	18 AAM19582	Human apoptosis in
33	431.5	5.9	604	19 AAM69295	Human H1AP-1 prote
34	427.5	5.8	602	18 AAM19585	Mouse apoptosis in
35	407	5.6	497	21 AAY59451	Human XIAP protein
36	403	5.5	497	18 AAM19581	Human apoptosis in
37	403	5.5	497	19 AAM69294	Human XIAP protein
38	403	5.5	497	21 AAY9985	Human X-linked inh
39	354	4.8	642	22 AAM25640	Human protein sequ
40	340.5	4.7	498	17 AAM04583	Human inhibitor of
41	336	4.6	498	22 AAB62863	Drosophila melanog
42	335	4.6	498	18 AAM19748	Human secreted pro
43	320	4.4	60	21 AAG01849	Angiotensin conver
44	318.5	4.4	306	22 AAU02925	
45	304.5	4.2	438	22 AAB48191	Drosophila mutant

ALIGNMENTS

RESULT 1
AAM20032
ID AAM20032 standard; Protein; 1403 AA.
XX
AC AAM20032;
XX
XX 06-OCT-1997 (first entry)
XX
DE Neuronal apoptosis inhibitor protein (NAIP).
XX
KW Neuronal apoptosis inhibitor protein; NAIP; diagnosis;
KW therapy; cancer; AIDS; amyotrophic lateral sclerosis;
KW spinal muscular atrophy.
XX
XX Homo sapiens.
OS
XX
XX W09726331-A2.
PN
XX 24-JUL-1997.
PD
XX
XX 17-JAN-1997; 57MO-IB00142.
PF
XX
XX 19-JAN-1996; 96GB-0001108.
PR
XX
XX (UYOT-) UNIV OTTAWA.
PA
XX
XX Korreluk RG, Mackenzie AE, Robertson G, Roy N, Tamai K;
PI WPT. 1997-38535/35.
DR N-PSDB: AAT71265.
XX
XX New neuronal inhibitor of apoptosis - useful for diagnosing and
PT treating, e.g. cancer, AIDS or amyotrophic lateral sclerosis
XX

PS Claim 41; Fig 6A-I; 102pp; English.

XX Novel human neuronal apoptosis inhibitor protein (AAW20032), or NAIP,
 CC is a negative regulator of apoptosis, partic. neuronal apoptosis
 CC and, when deficient or absent, contributes to neurodegenerative
 CC phenotypes such as spinal muscular atrophy (SMA) and amyotrophic
 CC lateral sclerosis. Its amino acid sequence was deduced from a
 CC cDNA clone (AA71265) obt. from a human foetal spinal cord cDNA
 CC library. NAIP polypeptides, esp. those containing at least two
 CC BIR (baculovirus IAP repeat) domains, can be expressed in host
 CC vector systems and used to increase or induce apoptosis in host
 CC treatment of AIDS, neurodegenerative disease, amyloidopathic
 CC syndromes or ischemic injury, to screen for (anti)agonists, or to
 CC produce antibodies useful for inhibiting apoptosis.

Sequence 1403 AA:

Query Match 100.0%; Score 7308; DB 18; Length 1403;
 Identical Similarity 100.0%; Pred. No. 0;
 Matches 1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MATGQKASDERISGFDHNLPELSALLGLDAVOLAKELSEEROKRAKMGKGYNSOMRSE 60
 1 matgqkasderisgfdhnlpe lsallgl davg lkelesee rorkrakmgkgy nsomrse 60
 61 AKRLKTFVTYEPYSSWIPOEMAAGFYGVKSGIQCCSLIFGAGLTRLPEDHKRF 120
 61 akrlk tftvtyep ysswi poema agfygv ksgiqcc slifga gltrlp edhkrf 120
 121 HPDCGLLNKKDVGNIADYDIRYKNSRLRGKMKRYOEENARLASFNNMFYVQSGSPV 180
 121 hpdc gl llnk kdvgn iady diry knsrl rgkm kyoe enar lsfnn mfyv qsgspv 180
 181 LSEAGVFENGKDYQVQCCSCCGCAGNMEEGDDPKWEHAKWPECELRKSKSEETROYI 240
 181 lseag vfeng kdyv qccsc cgcag nmeeg ddpk wehak wpece lrrk skse etroyi 240
 241 Iseagfvfctgkydvtvcfcscgcagcignweegddpkwehakekfrpcetlrrskseetlcy 240
 241 is eagfv fctg kydv tvcfc scgc agcign weeg ddpk wehak ekrpc etlrr skse etlcy 240
 301 OSYKGFVDITGEHFVNSVWQRELPMAAYCNDISFAYEELRLDSFKDMPREAVAVALA 300
 301 osykg fvdit ge hfvns vwqre lpm aayc ndisf ayeel rlds fkdmp reav avala 300
 301 KAGFYGINDIYQCFSCGCLLEKWOEGDDPLDDHTRCPNCPNCPNCKSSAEVTPLOS 360
 301 kagf ygind iycf scgcl lekwo egdd pldd htrc pncpnc pncpnc kssae vtplos 360
 361 KAGFYGINDIYQCFSCGCLLEKWOEGDDPLDDHTRCPNCPNCPNCKSSAEVTPLOS 360
 361 kagf ygind iycf scgcl lekwo egdd pldd htrc pncpnc pncpnc kssae vtplos 360
 361 RGELCELETTSESNEEDSIAVGPIVPEMAOCEAOEAFODAKNLEOLRAAVTSAFRRHS 420
 361 rgel cel ettes eneed s iavg pivpe maoc eaoe afoda knle olra avtsa frrhs 420
 421 LLDISSDLATDHLGDDLSIAKSHISKVQBPVLPVFEVGNLNSVMVEGEAGSGTVLL 480
 421 lldiss dlat dhl gddls iaksh iskvpv lpvfe vgnl nsvm veger agsgt vll 480
 481 Lldissdlatdhl gddls iaksh iskvpv lpvfe vgnl nsvm veger agsgt vll 480
 481 KKIARLMAAGCCPLNRFQVLYSLSTRPDEGLASTICDOLLEKRGVTECKMNIITO 540
 481 kkiar lmaag ccpl nrfqv ly slstr pdegl astic dolle krgv teckm niito 540
 541 KKIARLMAAGCCPLNRFQVLYSLSTRPDEGLASTICDOLLEKRGVTECKMNIITO 540
 541 kkiar lmaag ccpl nrfqv ly slstr pdegl astic dolle krgv teckm niito 540
 541 OKNOVLFLLDYKEICISIPVYIKLQKHNLSRTCLLAFTNRARORDRRLLEITLITIK 600
 541 okno vlfll dyke icis ipvy iklq khnls r tclla ftnr arord rrlle itlitik 600
 601 APEFYNTVCIRKLPSNNMTRLRKFMVYFGKNSLOKIOKTLFLFAALCAHMFQYPEDPS 660
 601 apefy ntv cirkl p s n n m t r l r k f m v y f g k n s l o k i o k t l f l f a a l c a h m f q y p e d p s 660
 661 APEFYNTVCIRKLPSNNMTRLRKFMVYFGKNSLOKIOKTLFLFAALCAHMFQYPEDPS 660
 661 apefy ntv cirkl p s n n m t r l r k f m v y f g k n s l o k i o k t l f l f a a l c a h m f q y p e d p s 660
 721 EDLTMCLMSFTAQRLRPYRFLSPAQOFLAGMRLILALSDSQEODGLYHLQINS 780
 721 edl t m c l m s f t a q r l r p y r f l s p a q o f l a g m r l i l a l s d s q e o d g l y h l q i n s 780
 721 EDLTMCLMSFTAQRLRPYRFLSPAQOFLAGMRLILALSDSQEODGLYHLQINS 780
 721 edl t m c l m s f t a q r l r p y r f l s p a q o f l a g m r l i l a l s d s q e o d g l y h l q i n s 780

QY 781 PMATVSAVNNFLNVSSSLPSTKAGPKIVSHLLHLVDNKNESLENISENDYLRKHOPETSLQ 840
 DB 781 pmatv savnn flnv sssl pstk agpk ivsh llhl vdn knes lenise ndy l r kh o p e t s l q 840
 QY 841 MOLLRGMOICPQAVRSNMSSEHLVLAALTAQVSNVTAAGSPFLQFLOCTTLTGALNT 900
 DB 841 m o l l r g m o i c p q a v r s n m s s e h l v l a a l t a q v s n v t a a g s p f l o c t t l t g a l n t 900
 QY 841 m o l l r g m o i c p q a v r s n m s s e h l v l a a l t a q v s n v t a a g s p f l o c t t l t g a l n t 900
 QY 901 QYFDDHPELSLDRSIRHPTRNKNTPRAHSVLETGCRDQSVFPFDIDQVAFEPENEM 960
 DB 901 q y f d d h p e l s l d r s i r h p t r n k n t p r a h s v l e t g c r d q s v f p f d i d q v a f e p e n e m 960
 QY 961 ERNLEKEEDNVKSYMDKORASPOLSTGYWKLSPKQYKIRPLEVDVNDIDVYQOMLETL 1020
 DB 961 ernle keednv ksy m d k o r a s p o l s t g y w k l s p k q y k i r p l e v d v n d i d v y q o m l e t l 1020
 QY 1021 MTFVSAQRIELHNSRGFTESIRPALERISKASYKCSISKLELSAAEQELTLPLSE 1080
 DB 1021 m t f v s a q r i e l h n s r g f t e s i r p a l e r i s k a s y k c s i k l e l s a a e q e l t l p l s e 1080
 QY 1081 SLEVSGTISODQIFPRLDKFLCLAKLSYDLEGNINVSIVIPPEFPNPHHEKILLIOISA 1140
 DB 1081 sle v s g t i s o d q i f p r l d k f l c l a k l s y d l e g n i n v s i v i p p e f p n p h h e k i l l i o i s a 1140
 QY 1141 EYDPSKLVKLIQNSPULHYPHLKCNFSDGSLMTLVSCKRIEIRFSDSFPQAVFVA 1200
 DB 1141 ey d p s k l v k l i q n s p u l h y p h l k c n f s d g s l m t l v s c k r i e i r f s d s f p q a v f v a 1200
 QY 1201 SLNFTSLILNLEGOFPDEFTSEKFAVITGSLNSNEELTPRGDDITYAVAKLIIOCCO 1260
 DB 1201 sl n f t s l i l n l e g o f p d e f t s e k f a v i t g s l n s n e e l t p r g d d i t y a v a k l i o c c o 1260
 QY 1261 QJHCLRVLSFFKTLNDDSVELAKVAISGQKLENKLSINRKITEEGYRNFQALDNM 1320
 DB 1261 q j h c l r v l s f f k t l n d d s v e l a k v a i s g q k l e n k l s i n r k i t e e g y r n f q a l d n m 1320
 QY 1321 PNLGELDLSRFTETCIRKAOATVKSLSQCVLRPLRIRLNMKLSMLDADADILNVMER 1380
 DB 1321 p n l g e l d l s r f t e t c i r k a o a t v k s l s q c v l r p l r i r l n m k l s m l d a d a d i l n v m e r 1380
 QY 1381 HPQSKYLTILQKWTLPSPPIOK 1403
 DB 1381 h p q s k y l t i l q k w t l p s p p i o k 1403

RESULT 2
 AAY14079
 ID AAY14079 standard; Protein; 1403 AA.
 AC AAY14079;
 XX
 DT 20-JUL-1999 (first entry)
 XX
 DE Gonadotropic hormone protein sequence.
 XX
 KM Gonadotropic hormone; excessive ovulation animal; transgenic animal;
 XX totipotent cell; somatic cell chromosome.
 OS Homo sapiens.
 PN JPI1113444-A.
 PD 27-APR-1999.
 XX
 PF 14-OCT-1997; 97JP-0280830.
 XX
 PR 14-OCT-1997; 97JP-0280830.
 XX
 PA (KAGA-) KAGAKU GIUTSU SHINKO JIGODAN.
 PA (SAKA/) SAKAI H.
 XX
 DR WPI: 1999-320709/27.

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OM protein - protein search, using sw model

Run on: September 30, 2002, 15:03:59 : Search time 16.67 Seconds
(without alignments)
3258.760 Million cell updates/sec

Title: US-09-830-338-1
Sequence: 1 MATQKASERISQFDHNL.....SKYTLTKWLPSPITCK 1403

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	7308	100.0	1403 1	B1R1_HUMAN
2	4956	67.8	1403 1	B1R1_MOUSE
3	4919	67.3	1447 1	B1R2_MOUSE
4	4885	66.8	1403 1	B1R2_MOUSE
5	4811	65.8	1403 1	B1R2_MOUSE
6	4796.5	65.6	1402 1	B1R2_MOUSE
7	654	8.9	1024 1	CARC_HUMAN
8	462	6.3	618 1	B1R3_MOUSE
9	457.5	6.3	612 1	B1R3_MOUSE
10	440	6.0	600 1	B1R2_MOUSE
11	436.5	6.0	604 1	B1R2_MOUSE
12	431.5	5.9	496 1	B1R4_MOUSE
13	416.5	5.7	496 1	B1R4_MOUSE
14	407	5.6	497 1	B1R4_MOUSE
15	388	5.3	611 1	B1R2_MOUSE
16	335	4.6	498 1	B1R2_MOUSE
17	326	4.5	358 1	PIAP_PIG
18	303.5	4.2	275 1	IAP_GYPC
19	301	4.1	438 1	IAP1_DROME
20	293.5	4.0	268 1	IAP3_NPOV
21	201.5	2.8	1062 1	NAL1_HUMAN
22	198	2.7	1473 1	NAL1_HUMAN
23	194.5	2.7	997 1	B1R1_SCHPO
24	192	2.6	1453 1	VP15_YEAST
25	182	2.5	953 1	CAR4_HUMAN
26	180.5	2.5	3210 1	CENF_HUMAN
27	175.5	2.4	275 1	IAP1_NPOV
28	167	2.3	4540 1	DYHC_PART2
29	166.5	2.3	1040 1	CARE_HUMAN
30	165.5	2.3	1315 1	CHAO_DROME
31	164.5	2.3	286 1	IAP1_NPVAC
32	163	2.2	239 1	ZFP_IRV6
33	163	2.2	1041 1	TLR8_HUMAN

34	161	2.2	2300 1	CYAA_NEUCR
35	160	2.2	140 1	B1R5_MOUSE
36	159	2.2	4639 1	DYHC_DROME
37	157	2.1	2014 1	IUV7_YEAST
38	156.5	2.1	1174 1	YJ11_YEAST
39	155.5	2.1	1692 1	CYAA_SCHPO
40	155	2.1	142 1	B1R5_HUMAN
41	155	2.1	4092 1	DYHC_YEAST
42	154	2.1	142 1	B1R5_RAT
43	154	2.1	1118 1	YPT4_CAEEL
44	153	2.1	784 1	TLR2_BOVIN
45	152.5	2.1	2663 1	CENE_HUMAN

ALIGNMENTS

RESULT 1
ID B1R1_HUMAN STANDARD: PRT: 1403 AA.
AC Q13075: Q13730; Q99796; Q75857;
BT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1 (neuronal apoptosis
inhibitory protein).
GN B1R1 OR NAIP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=95112344; PubMed=7813013;
RA Roy N., Mahadevan M.S., McLean M., Shuttler G., Yaraqhi Z.,
RA Farahani R., Baird S., Besner-Johnston A., Lefebvre C., Kang X.,
RA Salih M., Aubry H., Tamai K., Guan X., Ioannou P., Crawford T.O.,
RA de Jong P.J., Surh L., Ikeda J., Korneluk R.G., Mackenzie A.;
RT "The gene for neuronal apoptosis inhibitory protein is partially
deleted in individuals with spinal muscular atrophy.";
RL Cell 80:167-178(1995).
RN [2]
RP SEQUENCE FROM N.A., AND REVISIONS.
RC TISSUE=Brain;
RX MEDLINE=96163755; PubMed=9503025;
RA Chen Q., Baird S.D., Mahadevan M., Besner-Johnston A., Farahani R.,
RA Xuen J.-Y., Kang X., Lefebvre C., Ikeda J.-E., Korneluk R.G.,
RA Mackenzie A.E.;
RT "Sequence of a 131-kb region of 5q13.1 containing the spinal muscular
atrophy candidate genes SMN and NAIP.";
RL Genomics 48:121-127(1998).
RN [3]
RP SEQUENCE OF 386-623 FROM N.A.
RA der Steege G., Draalijers T.G., Grootscholten P.M., Olinga J.,
RA Anzeveno R., Vellona I., Brahe C., Scheffer H., van Ommen G.J.B.,
RA Buys C.H.C.M.;
RT Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 222-1403 FROM N.A.
RA Jones K., Graves T., McPherson J.;
RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP FUNCTION.
RC TISSUE=Liver;
RX MEDLINE=96149249; PubMed=8552191;
RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Cherton-Horvat G.,
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
family of IAP genes.";
RL Nature 379:349-353(1996).
CC -!- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOTOR NEURONS, BUT NOT IN SENSORY
 CC NEURONS. FOUND IN LAYER AND PLACENTA, AND IN A LESSER EXTENT IN
 CC SPINAL CORD.
 CC -1- DISEASE: MUTATED OR DELETED FORMS OF NAIP HAVE BEEN FOUND IN
 CC INDIVIDUALS WITH SPINAL MUSCULAR ATROPHY TYPE I (SMA TYPE I). SMAS
 CC ARE FATAL AUTOSOMAL RECESSIVE DISORDERS SUBCLASSIFIED AS TYPE I
 CC (WERNICKE-HOFFMANN DISEASE), TYPE II (INTERMEDIATE FORM), AND TYPE
 CC III (WOLFF-PARK-KUDELBERG-WELANDER DISEASE) BASED UPON THE AGE OF
 CC ONSET AND CLINICAL SEVERITY. THESE NEURODEGENERATIVE DISORDERS ARE
 CC CHARACTERIZED BY DEGENERATION OF LOWER MOTOR NEURONS, LEADING TO
 CC PROGRESSIVE PARALYSIS MUSCULAR ATROPHY. CONCERNS 1 IN 6000
 CC MEMBERS.
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL: U19251; AAC52045.1; -
 CC DR EMBL: U80017; AAC52047.1; -
 CC DR EMBL: U21913; AAA64504.1; -
 CC DR EMBL: AC005031; AAC62261.1; -
 CC DR HSSP: Q13490; 10BH.
 CC DR MIM: 600355; -
 CC DR InterPro: IPR001370; BIR.
 CC DR Pfam: PF00653; BIR; 3.
 CC DR SMART: SM00238; BIR; 3.
 CC DR PROSITE: PS01282; BIR_REPEAT_1; 3.
 CC DR PROSITE: PS0143; BIR_REPEAT_2; 3.
 CC DR PROSITE: PS00837; NACHT; 1.
 CC KM Apoptosis: Repeat.
 CC FT REPEAT 60 127 BIR 1.
 CC FT REPEAT 159 227 BIR 2.
 CC FT REPEAT 278 345 BIR 3.
 CC FT DOMAIN 464 758 NACHT.
 CC FT CONFLICT 222 223 PK -> YR (IN REF. 4).
 CC FT CONFLICT 386 387 VP -> ST (IN REF. 3).
 CC FT CONFLICT 535 535 Y -> H (IN REF. 3).
 CC FT CONFLICT 553 553 Y -> H (IN REF. 3).
 CC FT CONFLICT 1228 1231 MISSING (TN REF. 4).
 CC SQ SEQUENCE 1403 AA: 159613 MW: 566304C134DA5B64 CRC64;
 CC
 CC Query Match Best Local Similarity 100.0%; Score 7308; DB 1; Length 1403;
 CC Matches 1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 MATQOKASDERISQFDHNLPELSALLGLDAVOYLAKELKEEEOKEKAKMOKYNSOMSE 60
 CC DB 1 MATQOKASDERISQFDHNLPELSALLGLDAVOYLAKELKEEEOKEKAKMOKYNSOMSE 60
 CC QY 61 AKRLKFTVTEPEVSSMTPEOMAAGFTYGVNSGIQCFCCLILFGAGITRLPIEDHKRF 120
 CC DB 61 AKRLKFTVTEPEVSSMTPEOMAAGFTYGVNSGIQCFCCLILFGAGITRLPIEDHKRF 120
 CC QY 121 HPCCGFLNKNDVGNIAKYDIRVKNLSRLGGKMKRYOEERARLASFRNMPYVGISPCV 180
 CC DB 121 HPCCGFLNKNDVGNIAKYDIRVKNLSRLGGKMKRYOEERARLASFRNMPYVGISPCV 180
 CC QY 181 LSEAGVFPTGKODTVOCFSCGCLCNMEGDDPKWEHAKNPKCEFLRSKSSSEITQYI 240
 CC DB 181 LSEAGVFPTGKODTVOCFSCGCLCNMEGDDPKWEHAKNPKCEFLRSKSSSEITQYI 240
 CC QY 241 QSYKCFVDITGEHFVNSVWQRELPMASAYCNDSTFAYEEELRDSFKDMPRESAVGAALA 300
 CC DB 241 QSYKCFVDITGEHFVNSVWQRELPMASAYCNDSTFAYEEELRDSFKDMPRESAVGAALA 300
 CC QY 301 KAGLFYTGIDKIYVOCFSCGCLLEKWEQGDPLDHTRCFPNCPFLQNMKMSAEVTPDDLOS 360
 CC DB 301 KAGLFYTGIDKIYVOCFSCGCLLEKWEQGDPLDHTRCFPNCPFLQNMKMSAEVTPDDLOS 360

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 QY 361 KEELCELETTSESNELEDSIAVPIVPMAGBAOMQOKNLEOLRAAYTSASFRHMS 420
 DB 361 KEELCELETTSESNELEDSIAVPIVPMAGBAOMQOKNLEOLRAAYTSASFRHMS 420
 QY 421 LLDISSDLATHLGCDLSTASKHSKISRPVEPLVPEVGNLSVNCVGEAGSGRTYVL 480
 DB 421 LLDISSDLATHLGCDLSTASKHSKISRPVEPLVPEVGNLSVNCVGEAGSGRTYVL 480
 QY 481 KKIPIFMAAGCCPLLNRFOLVFLYLSSTPRDEGLASIIICDOLKEGSSVEMKRNITQ 540
 DB 481 KKIPIFMAAGCCPLLNRFOLVFLYLSSTPRDEGLASIIICDOLKEGSSVEMKRNITQ 540
 QY 541 QLNQOVFLLDYKEICISIPQVIGKLIQKNHSRCLLAVENTNARDIRRYLETILEIK 600
 DB 541 QLNQOVFLLDYKEICISIPQVIGKLIQKNHSRCLLAVENTNARDIRRYLETILEIK 600
 QY 601 AFPEYNTVCLIRKLFESHNTRLKKEVYFGKNQSLQIKTPEFLVAATCAHMPQPPDPS 660
 DB 601 AFPEYNTVCLIRKLFESHNTRLKKEVYFGKNQSLQIKTPEFLVAATCAHMPQPPDPS 660
 QY 661 FDDVAVFKSYMERTSLRNKATAEILKATVSSGELATLGFSCCFEPPNDLAEAGVED 720
 DB 661 FDDVAVFKSYMERTSLRNKATAEILKATVSSGELATLGFSCCFEPPNDLAEAGVED 720
 QY 721 EDLTMCIMSKFTAORLPPRYRFLSPAFOELAGNRLTELLDSROEQHODGLYHLQIOMS 780
 DB 721 EDLTMCIMSKFTAORLPPRYRFLSPAFOELAGNRLTELLDSROEQHODGLYHLQIOMS 780
 QY 781 PMMTVSANINFLNVSSLPSTKAGPKIVSHLHLVYDKESLEMINSENDYLYKHQPEISLO 840
 DB 781 PMMTVSANINFLNVSSLPSTKAGPKIVSHLHLVYDKESLEMINSENDYLYKHQPEISLO 840
 QY 841 MOLLGLMQLCPOAFVFSVSEHLVYLAKTAVQSNVAAVSPVLOFLOGRTLTGALNL 900
 DB 841 MOLLGLMQLCPOAFVFSVSEHLVYLAKTAVQSNVAAVSPVLOFLOGRTLTGALNL 900
 QY 901 QYFPDHEISLSLRSIHPIRGNKTSBRAHFSVLETCFDPKSOVPTTIDODYASAFENNEW 960
 DB 901 QYFPDHEISLSLRSIHPIRGNKTSBRAHFSVLETCFDPKSOVPTTIDODYASAFENNEW 960
 QY 961 ERNLAEKEDVAKSYMOMORASPDLSGTWKLSPYQYKIPCLEVDVNDIDVVGDMLEIL 1020
 DB 961 ERNLAEKEDVAKSYMOMORASPDLSGTWKLSPYQYKIPCLEVDVNDIDVVGDMLEIL 1020
 QY 1021 MTFVSAORIEHLNANSRGFTIESIRPALELSKASVTKCSI SKLELSAAEOELTLTLPSTLE 1080
 DB 1021 MTFVSAORIEHLNANSRGFTIESIRPALELSKASVTKCSI SKLELSAAEOELTLTLPSTLE 1080
 QY 1081 SLEVSQGTIOSQOQIPPNLDKFLCLKELSVDLEGNINPVSVPPEEFPNFMHEKLLQISA 1140
 DB 1081 SLEVSQGTIOSQOQIPPNLDKFLCLKELSVDLEGNINPVSVPPEEFPNFMHEKLLQISA 1140
 QY 1141 EYDPSKLYVLIONSNNLHVFLKCNFSDFOSLMTNLVSCKLTLEIKFSNFSFOANPFA 1200
 DB 1141 EYDPSKLYVLIONSNNLHVFLKCNFSDFOSLMTNLVSCKLTLEIKFSNFSFOANPFA 1200
 QY 1201 SLNPNFISKLINLEGGQFPDEETSEKRAYILGSLSNLEELILPTGDIYRVAKLIIQCO 1260
 DB 1201 SLNPNFISKLINLEGGQFPDEETSEKRAYILGSLSNLEELILPTGDIYRVAKLIIQCO 1260
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 DB 1261 QLHCLRYLSFPKTLINDSVEIAKVALISGGFQKLEMLKISINHKTITEEGRYRFPALDNM 1320
 QY 1321 PNLQELDISRHFECEIAQATYKLSQCVLRLPRLIRLNLMSWLLDDADIALNVYKER 1380
 DB 1321 PNLQELDISRHFECEIAQATYKLSQCVLRLPRLIRLNLMSWLLDDADIALNVYKER 1380
 QY 1381 HPQSKYITLQKAILPFSPIQK 1403
 DB 1381 HPQSKYITLQKAILPFSPIQK 1403


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Db 961 EKNLSSENEETIKSINKNIFLOPPKISSGTMKLSRCKIPRELEVGYNMGADALLOV 1020
OY 1021 MTFVFSASORIEHLNHSRGLIESIRPALELSKASVTCGSKISKELSAABDELLITPSIE 1080
Db 1021 MEVFSASOSIERLSDSSGFLIESIRPALELSKASVTCGSKISKELSAABDELLITPSIE 1080
OY 1081 SLEVGSTIQSDODIFPNIDKFLCKELSVDEGINVFSYIPPEPFPNFMKELIIOISA 1140
Db 1081 SLEVGSTIQSDODIFPNIDKFLCKELSVDEGINVFSYIPPEPFPNFMKELIIOISA 1140
OY 1141 EYDSKVLKVLIONSPNLHVFLKCNFSDGSLMTLVSCKLFTEKTSDFQAVPVYA 1200
Db 1141 EYDSKVLKVLIONSPNLHVFLKCNFSDGSLMTLVSCKLFTEKTSDFQAVPVYA 1200
OY 1201 SLPEPISLKLNLBEGQFDEETSEKAVILGSLNTELLIPGDCGYRAVAKLIIQCC 1260
Db 1201 ILPEPISLKLNLBEGQFDEETSEKAVILGSLNTELLIPGDCGYRAVAKLIIQCC 1260
OY 1261 QLHCLRVLSFFKTLNDSDVVEIAKVAISGCTOKLEMLKLSINRITTEGGRNFPQALDN 1320
Db 1261 QLHCLRVLSFFKTLNDSDVVEIAKVAISGCTOKLEMLKLSINRITTEGGRNFPQALDN 1320
OY 1321 PNLOELDISRHTBECIKAOATTVKSLSDCVLRPLRLIAMLMSLDLADLALNVKMR 1380
Db 1321 PNLOELDISRHTBECIKAOATTVKSLSDCVLRPLRLIAMLMSLDLADLALNVKMR 1380
OY 1381 HQSKYVLTILQKWLIPSPRII 1401
Db 1381 HQSKYVLTILQKWLIPSPRII 1401
OY 1401 HQSKYVLTILQKWLIPSPRII 1401
Db 1401 HQSKYVLTILQKWLIPSPRII 1401

RESULT 3
BIRB_MOUSE STANDARD: PRT: 1447 AA.
AC 090UK4: 09R030: 009124;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 2.
GN Inhibitory protein 2.
OS Mus musculus (Mouse).
OC Birc3b OR Nalp2 OR Nalp-RS6.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang S., Scharf J.M., Growney J.D., Enditzzi M.G., Dietrich W.F.:
RT "The mouse Nalp gene cluster on Chromosome 13 encodes several distinct
RT functional transcripts."
RL Mamm. Genome 10:1032-1035(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE-99315342; PubMed-10384056;
RA Yaregahli Z., Dietz E., Gros P., Mackenzie A.:
RT "cDNA cloning and the 5' genomic organization of Nalp2, a candidate
RT gene for murine Legionella resistance."
RL Mamm. Genome 10:761-763(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-129/SV:
RA MEDLINE-99417674; PubMed-10486205;
RA Enditzzi M., Huang S., Scharf J.M., Kelter A.R., Wirth B.,
RA Kunzel L.M., Miller W., Dietrich W.F.:
RT "Comparative sequence analysis of the mouse and human Lgn1/SMA
RT interval."
RL Genomics 60:137-151(1999).
RN [4]
RP SEQUENCE OF 82-168 FROM N.A.
RC STRAIN-129/SV:
RX MEDLINE-97131520; PubMed-8975718;

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RA Scharf J.M., Damron D., Frisella A., Bruno S., Beggs A.H.,
RA Kunzel L.M., Dietrich W.F.:
RT "The mouse region syntenic for human spinal muscular atrophy lies
RT within the Lgn1 critical interval and contains multiple copies of Nalp
RT exon 5."
RL Genomics 38:405-417(1996).
CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
CC -----
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CC -----
DR EMBL: AF135489; MAD56761.1; -
DR EMBL: AF135490; MAD56762.1; -
DR EMBL: AF102871; AAC73002.1; -
DR EMBL: AF131205; MAD56759.1; -
DR EMBL: U66329; AAC52977.1; -
DR HSSP: Q13490; 108H
DR MGI: 1298226; Birc3b.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR_3.
DR SMART: SM00238; BIR_3.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS00837; NACHT; 1.
KW Apoptosis; Repeat; Multigene family.
FT REPEAT 127 BIR 1.
FT REPEAT 159 227 BIR 2.
FT REPEAT 278 345 BIR 3.
FT DOMAIN 508 802 NACHT.
FT CONFLICT 377 377 D -> G (IN REF. 3).
FT CONFLICT 403 403 L -> F (IN REF. 3).
FT CONFLICT 478 478 L -> I (IN REF. 3).
FT CONFLICT 540 540 N -> Y (IN REF. 3).
FT CONFLICT 862 862 K -> N (IN REF. 3).
FT CONFLICT 1079 1080 SD -> FN (IN REF. 3).
FT CONFLICT 1089 1089 R -> C (IN REF. 3).
FT CONFLICT 1115 1115 K -> E (IN REF. 3).
FT CONFLICT 1122 1122 T -> A (IN REF. 3).
FT CONFLICT 1136 1136 D -> E (IN REF. 3).
FT CONFLICT 1157 1157 S -> G (IN REF. 3).
FT CONFLICT 1167 1167 G -> R (IN REF. 3).
FT CONFLICT 1271 1271 F -> C (IN REF. 3).
SQ SEQUENCE 1447 AA; 164033 MW; 9FE6C6A73BAE60A2 CRC64;

Query Match 67.38; Score 4919; DB 1; Length 1447;
Best Local Similarity 65.48; Pred. No. 4,4e-284;
Matches 946; Conservative 180; Mismatches 277; Indels 44; Gaps 2;
OY 1 MAAOKASDERISOFDHNILPELSALGLDAVOLAKLEEEEOKRAMOGVNSORSE 60
Db 1 MAAOGEAVEEELICEFDDDLIVSELSTLLRVADLSYLRQOEDDHTRMKMKGFNSQRSE 60
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Db 61 AKRLKFTVTEPEYPSWIPOEMAAGFTYGVKSGIQCCSLIFGAGLTRLPJEDHKRF 120
OY 121 HPDCGFLKMDKGNATKADIRVKNLSRLRGKMYOESEARLASFPNPFYOGISPCV 180
Db 121 HPDCGFLKMDKGNATKADIRVKNLSRLRGKMYOESEARLASFPNPFYOGISPCV 180
OY 181 LSAAGVFTGKODTVQCCSGCGCLGNNEEGDDPKKHAKEFPKCEFLRSKSSSEETIY 240
Db 181 LSAAGVFTGKODTVQCCSGCGCLGNNEEGDDPKKHAKEFPKCEFLRSKSSSEETIY 240

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Qy 241 QSYKGFVDITGEHFVNVSQRELPNASAYCNDISFAYEELRLDSFKDMPRESAVGVALA 300
Db 241 QSYEGFLVHTGEHFVNVSRRRLPMVASACNDISFANERLMDTFRKDPHESPGAVELV 300
Qy 301 KAGLFYTGKIDVOGFCSSGGCLEKQEBDDPLDDHTRCFPKPCPIQNKSSAEVTPDLQS 360
Db 301 KAGLFYTGKIDVOGFCSSGGCEKMEKWDNPJEDHTKEFPNCVFLQTLKSSAEVTPALQS 360
Qy 361 RGELELETTSESNEEDSIAY----- 382
Db 361 HCALPEAMETTESNHDPAHAHSTVDVSPSEAOLEPSSVLYLCRDDHSEAPGRC 420
Qy 383 ----GPIVP--EMAQGEAQMFQEAKNLNEOLRAATYSAFRMSLIDISSDLATDHLGC 436
Db 421 CASSGTVPISPTDLSGEAQMOLDEARLSBQLRDYTKATFRMANLPEVYSLGTHLLSC 480
Qy 437 DLISAKSIKRVQEPVLVPEVFGMLNSVCEVSEAGSGKTVLLKIAFLMAAGCCPLIN 496
Db 481 DVSIISKHISQPVQSGTLTPEVFSMLNSVMCEVSEAGSGKTFKRIAFMAAGCCPLIN 540
Qy 497 RFOVFEYLSSTRDEGLASTICDQLLEKESVTEMKRNITQOLKNQVLFLLDYKEI 556
Db 541 RFOVFEYLSSTRDEGLASTICDQLLEKESVTEMKRNITQOLKNQVLFLLDYKEI 600
Qy 557 CSIPQVIGKLIQKNHLSRTCLLIAVRNARDIRRYLETILEIKAFPPYNTVCILKFLS 616
Db 601 ASLPQALHTLTKNVSLTCLLIAVHTNKVGRIRYLDTSLEIKFPPYNTVYARLFLS 660
Qy 617 HNMTRKRFMYFCKNOSLOKTPLEVAALICAMFQYPPDPSPDDVAVERKSYERLSL 676
Db 661 HDIMVRKRFINFGHEELQGIHKTPLEVAACVDMFNPSQAPQDALFRAYMQVYSL 720
Qy 677 RNMKATAEIKATVSSCGELATKGFSCCFEFPNDDDLAEAGVEDDELTCMLSKFTAORL 736
Db 721 KHKGAQKAPLOATVSSCGQALATGLFSSCFEPENSDILAEAGVEDDELTCMLSKFTAORL 780
Qy 737 RPEVFEYLSPAQOEFLAGKRLTLDSDROHODLGLYHLKQINSMPMTVSAVNNELVYS 796
Db 781 RPEVFEYLSPAQOEFLAAVRLTELSSDROEDDGLYLRQJNSLKLKMSIYHTEFLKYS 840
Qy 797 SLPTSKAGPKYVSHLHLVDNKESLENTSENDYLRKHOPEISLOMQLRGLMQICPOAYF 856
Db 841 SHPSKKAAPVYVSHLQVDEKESLENMSMEDYMKLHREALMTECRLGMLQPSRESFS 900
Qy 857 SWSVSHLVIALKTAYOSNTVAAGSPYLOFQOGLTTLGALNTLYFPDHPRESLSLSI 916
Db 901 LPTISNLRICLNFANHESNTVAAGSPVLLQFLGRITLDKVLSTQYFMDHPETLLLSLSI 960
Qy 917 HEPINGNTSPRAHPSVLETCFEDKSQVPTIDODYASAEFPMNEMERNLAEKEDVKSYPD 976
Db 961 KISLGNMNMVQORIDFSLIEKSPKQVPTIDODYALAFOPINEVOGNLSEKKHIIKKYED 1020
Qy 977 MORRASPDLSGTGYKWLSTKQYKIPCLLEVVDNDIVVGGDMLEILMTVVSASRIELAHNH 1036
Db 1021 MKHQIPLNISTGYKWLSTKQYKIPCLLEVQVNTGTGADADLLQVLMLEVVSASQISIEFRLSD 1080
Qy 1037 SRGFIESTIRPALELSKASVTKCSISKLELSAEQELLTLTLPLESLEVSGTQISODQIFP 1096
Db 1081 SSGFIESTIRPALELSKASVTKCSMRLELSRDQKLLTLTLPLOSLEVSETQMDQLFPH 1140
Qy 1097 NLDKFLCLKELSVDLEGNINVFSPVPEEPNFEHMEKLLIQISABYDSKLVKLLQNSPN 1156
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Qy 1157 LHVFLKKNFSDSGSLMTMLVSCKKLTKIKFSDFQVAPPVVVALPFIISKIINTLEQ 1216
Db 1201 LHVFLKKNFSDSGSLMTMLVSCKKLTKIKFSDFQVAPPVVVALPFIISKIINTLEQ 1260
Qy 1217 QPPDEETSEKFAVILGSLSNLEELILTPGDIYRAKLLIQCCQOLHLCRAVLSPFKTLD 1276
Db 1261 QPPDEETSEKFAVILGSLSNLEELILTPGDIYRAKLLIQCCQOLHLCRAVLSPFKTLD 1320
Qy 1277 DSVETIARVAISGFGOKLENLKLSTNHKITEBGRNFFQALDNMPNLQELDISRHETECI 1336

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Db 1321 DSVETIARVATGSGFGOKLENLDTLTKHKTTEBGRNFFQVLDNPLNKLNDISRHETECI 1380
Qy 1337 KQATTVVSLSCVLRRLRLRLNLNLSMLDADIALNWKERKRPQSKYLTLLQKALP 1396
Db 1381 QIQAITVALGCVSRPLSLRLGLMSLWLBEDEDIKVINDYKERRHQRSLTVHWRVVP 1440
Qy 1397 FSPITOK 1403
Db 1441 FSPVITOK 1447

RESULT 4
BIRE_MOUSE
ID BIRE_MOUSE STANDARD: PRT: 1403 AA.
AC Q9R016; Q9R029; P81703; 009122; 009121;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1e (Neuronal apoptosis
inhibitory protein 5).
CN BIRC1 OR NAIP5 OR NAIP-RS3.
OS Mus musculus (Mouse).
OC Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99431676; PubMed-10501978;
RA Huang S., Scharf J.M., Growney J.D., Endrizzi M.G., Dietrich W.F.;
RT "The mouse Naip gene cluster on Chromosome 13 encodes several distinct
functional transcripts."
RL Mamm. Genome 10:1032-1035(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-129/SV;
RC MEDLINE-9941674; PubMed-10486205;
RA Endrizzi M., Huang S., Scharf J.M., Kelter A.R., Wirth B.,
RA Kunkel L.M., Miller W., Dietrich W.F.;
RT "Comparative sequence analysis of the mouse and human Iqnl1/SMa
interval."
RL Genomics 60:137-151(1999).
RN [3]
RP SEQUENCE OF 82-168 FROM N.A.
RX STRAIN-129/SV;
RC MEDLINE-97131520; PubMed-8975718;
RA Scharf J.M., Damron D., Fritsella A., Bruno S., Beggs A.H.,
RA Kunkel L.M., Dietrich W.F.;
RT "The mouse region syntenic for human spinal muscular atrophy lies
within the Iqnl1 critical interval and contains multiple copies of Naip
exon 5."
RL Genomics 38:405-417(1996).
CC -I- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.
CC -I- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -I- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
CC -----
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CC -----
DR EMBL: AF135492; AAD56764.1; -
DR EMBL: AF131205; AAD56760.1; -
DR EMBL: U66326; AAC52974.1; -
DR HSSP: Q13490; 10BH.
DR MGP: MGI-1298220; Birc1e.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.

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DR PROSITE; PS01282; BIR_REPEAT_1; 2.
 DR PROSITE; PS50143; BIR_REPEAT_2; 3.
 DR PROSITE; PS50837; NACHT; 1.
 KW Apoptosis; Repeat: Multigene family.
 FT REPEAT 60
 FT REPEAT 127
 FT REPEAT 159
 FT REPEAT 227
 FT REPEAT 278
 FT REPEAT 345
 FT REPEAT 464
 FT REPEAT 759
 FT REPEAT 92
 FT REPEAT 144
 FT REPEAT 242
 FT REPEAT 472
 FT REPEAT 516
 FT REPEAT 521
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 FT REPEAT 1242
 FT REPEAT 1276
 FT REPEAT 1403
 AA: 159695 MW: B27F645043BCECA2 CRC64;

Query Match Best Local Similarity 66.8%; Score 4885; DB 1; Length 1403;
 Matches 947; Conservative 167; Mismatches 286; Indels 2; Gaps 2;

QY 1 MATOAKASDERISOFHNLPELSALLGLDANOAKLELEEDQERAKKQKQNSOMSE 60
 DB 1 MAHGESSEDRISIDYEFLEFLEALLGLDANOAKLELEEDQERAKKQKQNSOMSE 60
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 DB 61 AKRKTATVTEPYSSWIPQEMAAGFYFYGVKSGIOCCSCSLILEGALTLRLPIEDHKE 120
 QY 121 HPDCGLFLNKDVGNIAKYDIAIRVKNLSRGLGKMKRYQDEARLASFRNMPFYVGISPCV 180
 DB 121 RPECEFLGCKDGNICKYDIAIRVKNLSRGLGKMKRYQDEARLASFRNMPFYVGISPCV 180
 QY 181 LSPAGFVFGKDDYVOCFSCGCGCLGNEEGDDPMKEHAKMPKCELFKSKSSSELTQYI 240
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 QY 241 QSYKGFVDITGEHFNVSNOVRELPMASAYCNDISFATYELRLDSFKDMPRESAVGAALA 300
 DB 241 QSYKGFVDITGEHFNVSNOVRELPMASAYCNDISFATYELRLDSFKDMPRESAVGAALA 300
 QY 301 KAGLFYTGKIDYVOCFSCGCGCLGNEEGDDPMKEHAKMPKCELFKSKSSSELTQYI 360
 DB 301 KAGLFYTGKIDYVOCFSCGCGCLGNEEGDDPMKEHAKMPKCELFKSKSSSELTQYI 360
 QY 361 RAGFYTGKIDYVOCFSCGCGCLGNEEGDDPMKEHAKMPKCELFKSKSSSELTQYI 420
 DB 361 RAGFYTGKIDYVOCFSCGCGCLGNEEGDDPMKEHAKMPKCELFKSKSSSELTQYI 420
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 DB 421 LLDLSSDLADHLLCDLSTASHKISKPYOEPLVPEVGNLSNWCYEGAGSKTYVL 480
 QY 481 KRIAFWASCCCLLRFLQVLYLSLSTTPDGLANTICAGLLGAGGCSSEVCLSSIQ 540
 DB 481 KRIAFWASCCCLLRFLQVLYLSLSTTPDGLANTICAGLLGAGGCSSEVCLSSIQ 540
 QY 541 QLNQVFLFLDDYKELISIPQVIGLQKMLSRFLCLITAVTRARARIRRYLETILEIK 600
 DB 541 QLNQVFLFLDDYKELISIPQVIGLQKMLSRFLCLITAVTRARARIRRYLETILEIK 600
 QY 601 AEPFNATVSLKRLKPSHNMTRLRKPMVYEGKNSLOKTYLFAVIAICAHMFQ-VFDP 659
 DB 601 AEPFNATVSLKRLKPSHNMTRLRKPMVYEGKNSLOKTYLFAVIAICAHMFQ-VFDP 659
 QY 660 SPDDVAVAKSKWERLSLNKATAEILKATVSSCGELAKGFFSCCFEFDNDLAEAGVDE 719
 DB 660 SPDDVAVAKSKWERLSLNKATAEILKATVSSCGELAKGFFSCCFEFDNDLAEAGVDE 719

DB 661 KFDQVTLFQSTWQYSLKATKATAEPLQATVSSCGQALTLGLFSSCFEFDNDLAEAGVDE 720
 QY 720 DEDLMCMKSKRTAOLRLRPFYFLSPAFQEFILAGMRLEILDSDROHODLGLYHKQIN 779
 DB 721 DEKTLTLMLKRTAOLRLRPFYFLSPAFQEFILAGMRLEILDSDROHODLGLYHKQIN 780
 QY 780 SPMTAVSNVNFELNVSSLPSTKAGPKIVSHLHLVKNKSLNENISENDYKHOPEISL 839
 DB 781 SPLKAINSENFIFLYVSSSHSSKAPVSVSHLQLDKESKSLNENISENDYKHOPEISL 840
 QY 840 QMOLLRGMOICPAYGSMVSEHLVLAATAVQSNVAVACSPFYLOPLQGRITGLALN 899
 DB 841 WQFVGRGMLVSPSSSVSEHLRLALFAVESNTVACSPFLQIRGTTALRLVFN 900
 QY 900 LQYFDPHESILSLRTHFIRGNKTSPPRAHFEVLTECDKQVPIQDDYASAFEPNE 959
 DB 901 LQYFDPHESILSLRTHFIRGNKTSPPRAHFEVLTECDKQVPIQDDYASAFEPNE 959
 QY 960 WERNIAEKEDNVKSYNDMORASPDULSTGYWKLSPKQYKIPCLEVDVNDIPVYGDMLEI 1019
 DB 960 WERNIAEKEDNVKSYNDMORASPDULSTGYWKLSPKQYKIPCLEVDVNDIPVYGDMLEI 1019
 QY 1020 LMTVFSASORIELHNSKGTESIRPALELSKASVTKCSISKLELSAEOELLTLPSL 1079
 DB 1020 LMTVFSASORIELHNSKGTESIRPALELSKASVTKCSISKLELSAEOELLTLPSL 1079
 QY 1080 ESLEVSCTIOSDDQIFPNLDKFLCKEISVYDEGNINVFYSIPEEPNFHMEKLLTOIS 1139
 DB 1080 OSLEVSCTIOSDDQIFPNLDKFLCKEISVYDEGNINVFYSIPEEPNFHMEKLLTOIS 1139
 QY 1140 AEDVPSKYLKLIQNSPNLHVFHLKCNFSDGSLMTMIVSKLTELKESDFQAVPV 1199
 DB 1140 TESDSLKLKLFQNPVHVFHLKCNFSDGSLMTMIVSKLTELKESDFQAVPV 1199
 QY 1200 ASLPNFSILKILNLEGOFPDEESSEKFAIYLSLSLELILPTDGIYVAKLTIQOC 1259
 DB 1200 NLPNFSILKILNLEGOFPDEESSEKFAIYLSLSLELILPTDGIYVAKLTIQOC 1259
 QY 1260 OOLHCLRLVFLKNDVSVEIAKVAISGFORLEMLKISIHKTTEGYSKNNFQALDN 1319
 DB 1260 LQPLCLRLVFLKNDVSVEIAKVAISGFORLEMLKISIHKTTEGYSKNNFQALDN 1319
 QY 1320 MPNLQELDIRHFEKTCIKAOATVKSISQCYLRLPLILNMLSWILDADDIALLNVAKE 1379
 DB 1320 LPNQELDIRHFEKTCIKAOATVKSISQCYLRLPLILNMLSWILDADDIALLNVAKE 1379
 QY 1380 RHPOSKYTLTLQKMLPFSPII 1401
 DB 1380 RHPOSKYTLTLQKMLPFSPII 1401

RESULT 5
 BIR_MOUSE
 ID BIR_MOUSE STANDARD; PRT; 1403 AA.
 AC 09JIB6; P81704; 009122; 009121;
 DT 16-OCT-2001 (rel. 40, Created)
 DT 16-OCT-2001 (rel. 40, Last sequence update)
 DT 01-MAR-2002 (rel. 41, Last annotation update)
 DE Baculoviral IAP repeat-containing protein 1f (Neuronal) apoptosis
 GN Inhibitory protein 6f.
 GN BIRCLF OR NAIP6 OR NAIP-RS4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclerogamath; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20414747; PubMed=10958627;
 RA Endrizzi M.G., Hadinoto V., Gromney J.D., Miller W., Dietrich W.F.:
 Genomic sequence analysis of the mouse Naip gene array.;
 RL Genome Res. 10:1095-1102(2000).
 RN [2]

RP SEQUENCE OF 82-168 FROM N.A.
 RC STRAIN-129/SVJ;
 RX MEDLINE-97131520: PubMed-8975718;
 RA Scharf J.M., Damron D., Fritsella A., Bruno S., Beggs A.H.,
 Kunkel L.M., Dietrich W.F.;
 RT "The mouse region syntenic for human spinal muscular atrophy lies
 within the Lgn1 critical interval and contains multiple copies of Nalp
 exon 5.";
 RL Genomics 38:405-417(1996).
 CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
 CC STIMULI.
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
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 CC -----
 DR EMBL: AF342431: AAF82751.1: -
 DR EMBL: U66327: AAC52975.1: -
 DR MGD: MGI:1298222: Birc1f.
 DR InterPro: IPR001370: BIR.
 DR Pfam: PF00653: BIR: 3.
 DR SMART: SM00238: BIR: 3.
 DR PROSITE: PS01282: BIR_REPEAT_1; 2.
 DR PROSITE: PS0143: BIR_REPEAT_2; 3.
 DR PROSITE: PS50837: NACHT: 1.
 DR Apoptosis: Repeat; Multigene family.
 FT REPEAT 60 127 BIR 1.
 FT REPEAT 159 227 BIR 2.
 FT REPEAT 278 345 BIR 3.
 FT DOMAIN 464 NACHT.
 SQ SEQUENCE 1403 AA: 159823 MW: 9DA912503358C4E9 CRC64:

Query Match 65.8% Score 4811: DB 1: Length 1403;
 Best Local Similarity 66.3% Pred. No. 1,1e-277;
 Matches 929; Conservative 174; Mismatches 237; Indels 2; Gaps 2;

QY 1 MATQOKASDERISQFDHNLPELSALLGLDAVOLAKLEEEBOKERAKQKGYNSOMSE 60
 DB 1 MAHGESESEIRIDELFEFLAELARSFGMLVOLAKSGEEDDHKRMKMGKGFNSOMSE 60
 QY 61 AKRLKLTFTYTPYSSWTPQEMAAAGFTYGVKSGIQFCGSLILFGAGLRLPTIEDHKRF 120
 DB 61 AKRLKLTFTYTPYSSWTPQEMAAAGFTYGVKSGIQFCGSLILFGAGLRLPTIEDHKRF 120
 QY 121 HPDCGFLLNKRVGNIAKIDIVKMLKSLRGCKMKRYOEBEARLASFRMPPYVGISICV 180
 DB 121 RPEEFLOGRKRVGNIGKIDIVKSPKMLRGCKMKRYOEBEARLASFRMPPYVGISICV 180
 QY 181 LSEAGFVFTGKQDVTQFCSCGGLGNMEBGDDPKKEHAKPKCEFLSKSKSSEETIYI 240
 DB 181 LSAAGFVFTGKQDVTQFCSCGGLGNMEBGDDPKKEHAKPKCEFLSKSKSSEETIYI 240
 QY 241 QSYGVFDVTGHEFVNSWQRELPMASAYCNDISFAYEELRLDSFKMPRESAVGVALA 300
 DB 241 QSYGVFDVTGHEFVNSWQRELPMASAYCNDISFAYEELRLDSFKMPRESAVGVALA 300
 QY 301 KAGLFTYGIKDIYOCFCGCGGLKMOEGDDPLDHTKCFPMCPFLONKSSAEVTPDLOS 360
 DB 301 KAGLFTYGIKDIYOCFCGCGGLKMOEGDDPLDHTKCFPMCPFLONKSSAEVTPDLOS 360
 QY 361 RAGLFTYGIKDIYOCFCGCGGLKMOEGDDPLDHTKCFPMCPFLONKSSAEVTPDLOS 360
 DB 361 RAGLFTYGIKDIYOCFCGCGGLKMOEGDDPLDHTKCFPMCPFLONKSSAEVTPDLOS 360
 QY 421 LLDISSDLATDHLGCDLSTASKHISKRVQEPVLYLPEVFGULNSVMYCEGAGSGKTVLL 480
 DB 421 LLDISSDLATDHLGCDLSTASKHISKRVQEPVLYLPEVFGULNSVMYCEGAGSGKTVLL 480

DB 421 LPEVCSLGTBHLGCDVSIISKHVQOPVQGLATIPVFSNLSVMYCEGAGSGKTVLL 480
 QY 481 KRIAPLWASGCCPLNRRQVLYLSLSTRDEGLASITICDOLKEGSSVTEMCRRNIIQ 540
 DB 481 KRIAPLWASGCCPLNRRQVLYLSLSTRDEGLASITITPOGLANITICDOLGAGCISEVCLSSSIO 540
 QY 541 QLNQOVFLDDYKEIGSPVYGVKLIQKNIHSLSCCLIAVTRNARIDRLRETLIEK 600
 DB 541 QLNQOVFLDDYKEIGSPVYGVKLIQKNIHSLSCCLIAVTRNARIDRLRETLIEK 600
 QY 601 APEFYNTVCIKLKLESHMTRLRKEMVTEGKNQSLQKIQKPLFYAAICAHMFO-YPPDP 659
 DB 601 EEPFYNTVCIKLKLESHMTRLRKEMVTEGKNQSLQKIQKPLFYAAICAHMFO-YPPDP 659
 QY 660 SPDDVAVRSVTERLSLNKKAETLKTAVSSCGGLAKGPFSCCFERNDDLAGVDE 719
 DB 660 SPDDVAVRSVTERLSLNKKAETLKTAVSSCGGLAKGPFSCCFERNDDLAGVDE 719
 QY 720 DEDLTMCMSKFTTAORLPFYRFLSPAFOEFLAGRLIEILDSDROEHODGLYLHAKIN 779
 DB 720 DEDLTMCMSKFTTAORLPFYRFLSPAFOEFLAGRLIEILDSDROEHODGLYLHAKIN 779
 QY 721 DYKLTFTPLMSKRTAORLPFYRFLSPAFOEFLAGRLIEILDSDROEHODGLYLHAKIN 780
 DB 721 DYKLTFTPLMSKRTAORLPFYRFLSPAFOEFLAGRLIEILDSDROEHODGLYLHAKIN 780
 QY 780 SPMAVTSAYNNFLNVTSSLPSTKACPKIVSHLHLVDNKESELENISENDVYLLKHOPEISL 839
 DB 780 SPMAVTSAYNNFLNVTSSLPSTKACPKIVSHLHLVDNKESELENISENDVYLLKHOPEISL 839
 QY 840 OMQLLRGLMOICPOAFVSMVSHLLVLAKTRAYOSNTYAAAGSPFYQILOQRTLTGLALN 899
 DB 840 OMQLLRGLMOICPOAFVSMVSHLLVLAKTRAYOSNTYAAAGSPFYQILOQRTLTGLALN 899
 QY 900 LOYFDPHESLILSLRHPFIRGNTPRAHPSVLETCFEDSKQVTTIOQDYAASAPNE 959
 DB 900 LOYFDPHESLILSLRHPFIRGNTPRAHPSVLETCFEDSKQVTTIOQDYAASAPNE 959
 QY 901 LEYFDHPSLILSLRHPFIRGNTPRAHPSVLETCFEDSKQVTTIOQDYAASAPNE 959
 DB 901 LEYFDHPSLILSLRHPFIRGNTPRAHPSVLETCFEDSKQVTTIOQDYAASAPNE 959
 QY 960 WERNLAEREDVWKSVMQORRASPDLSTGYMKSLEPKOYKIPCLEVDVNDIVYGDMDLEI 1019
 DB 960 WERNLAEREDVWKSVMQORRASPDLSTGYMKSLEPKOYKIPCLEVDVNDIVYGDMDLEI 1019
 QY 1020 LMTVFSASORIEILNHSRGFESTRPALELSKASVTGCSISKLELSAABDELLTLPSL 1079
 DB 1020 LMTVFSASORIEILNHSRGFESTRPALELSKASVTGCSISKLELSAABDELLTLPSL 1079
 QY 1080 ESLEVSCTIQSQDQIFPMLDKFLCKELSVDEGNINFSVYPEEFPNFMHHEKILIOIS 1139
 DB 1080 ESLEVSCTIQSQDQIFPMLDKFLCKELSVDEGNINFSVYPEEFPNFMHHEKILIOIS 1139
 QY 1140 AYEYDSKLVKLIQNSPNTLHVLKCNFSPDSGLMTMLVSCCKLTLEIKFSOSFOAVPV 1199
 DB 1140 AYEYDSKLVKLIQNSPNTLHVLKCNFSPDSGLMTMLVSCCKLTLEIKFSOSFOAVPV 1199
 QY 1200 ASLPNFIKLTILNLEGGQFPDEETSEKFAVITLGSISNLELTPDGTIVRAKILIOOC 1259
 DB 1200 ASLPNFIKLTILNLEGGQFPDEETSEKFAVITLGSISNLELTPDGTIVRAKILIOOC 1259
 QY 1260 QOLHCLRVLSFEKTLNDSVVEILAKVAISGCFOKLENLKLSINRKTIEGYRNFOALDN 1319
 DB 1260 QOLHCLRVLSFEKTLNDSVVEILAKVAISGCFOKLENLKLSINRKTIEGYRNFOALDN 1319
 QY 1320 MPNLOELDISRHFTFECIAQATVYKSLQCVLRPLRLINLWSLWLDADIALINVKE 1379
 DB 1320 MPNLOELDISRHFTFECIAQATVYKSLQCVLRPLRLINLWSLWLDADIALINVKE 1379
 QY 1380 RHPOSXYTITLQKWTLPSPPII 1401
 DB 1380 RHPOSXYTITLQKWTLPSPPII 1401

RESULT 6
 BIRG_MOUSE
 ID BIRG_MOUSE STANDARD: PRT: 1402 AA.
 AC Q90IB3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Baculoviral IAP repeat-containing protein 1g (Neuronal apoptosis
 GN BIRC6 OR NAIP7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP NCBI_TaxID=10090;
 RX SEQUENCE FROM N.A.
 RA MEDLINE=20414747; PubMed=10958627;
 RT Hadrizzi M.G., Hadinoto V., Gromey J.D., Miller W., Dietrich W.F.;
 RL "Genomic sequence analysis of the mouse Naip gene array.";
 CC Genome Res. 10:1095-1102(2000).
 CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
 CC SIGNALS.
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
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 CC -----
 DR EMBL: AF242433; AAF82749.1;
 DR MGD: MGI:1858256; Birc6l.
 DR InterPro: IPR001370; BIR.
 DR Pfam: PF00653; BIR; 3.
 DR SMART: SM00238; BIR; 3.
 DR PROSITE: PS01282; BIR_REPEAT_1; 2.
 DR PROSITE: PS0143; BIR_REPEAT_2; 3.
 DR PROSITE: PS50837; NACHT; 1.
 KM Apoptosis; Repeat; Multigene family.
 FT REPEAT 60 127 BIR 1.
 FT REPEAT 159 227 BIR 2.
 FT REPEAT 278 345 BIR 3.
 FT DOMAIN 464 759 NACHT.
 SQ SEQUENCE 1402 AA; 159662 MW; C1DFB3A359893E0D CRC64;

Query Match 65.68; Score 4796.5; DB: 1; Length 1402;
 Best Local Similarity 66.48; Pred. No. 7.9e-277;
 Matches 931; Conservative 171; Mismatches 297; Indels 3; Gaps 3;

Db 361 OVALPEATEETRESNNGDAAVHSTVVDLGRSEAQMFQEARSLSEQLRDYTTSTSCHN 420
 Qy 421 LDDISSDIAFDHLLCCDLSIAKHSKRPQEPVLPRVFGNLSVNCVCEGASGCTVLL 480
 Db 421 LREVCSSLTQDHLSCDVSIIKSHISQVQGALITPEVFSNLSVNCVCEGASGCTFL 480
 Qy 481 KRIAFILMAGCCPLINRQPLVYFSLSTRDEGLASIIQDQLLEKGVTECMQNI 540
 Db 481 KRIAFILMAGCCPLINRQPLVYFSLSTRDEGLASIIQDQLLEKGVTECMQNI 540
 Qy 541 QLNQVFLDLDDYECISIPQVIGLQKQNLRTCLLAFTNRARDIRLETILEIK 600
 Db 541 QLNQVFLDLDDYECISIPQVIGLQKQNLRTCLLAFTNRARDIRLETILEIK 600
 Qy 601 QLOHOFLELLDDYSGLSLPLQALHTLITKNYLFRTCLLAFTNRARDIRLETILEIQ 600
 Db 601 APEPVNTVCLIRKFSHNMRLEKRVYTGCKNOSLOKTPLFVAALICAHFO-YRDP 659
 Qy 601 EEPYNTVFLRKFPSIDITCYEKLITFSEKNKDIQGVKPLFVAANCDNMOMASAD 660
 Db 660 SPDDVAVFKSYMERLSLRKKAFAELIKATVSSCGELALKGFSCEFEFNDDLAAGVDE 719
 Qy 661 DFQDVTFLSHYQVLSIKYKATAESLQATVSSCGELALTLGFSCEFEFNDDLAAGVDE 720
 Db 720 DEDITWCLMSKFTYQRLRPFYFELSAPQEFLLAGRLIELDSDROBODLGLYHLKQIN 779
 Qy 721 DVKLTFLMSKFTYQRLRPFYFELSAPQEFLLAGRLIELDSDROBODLGLYHLKQIN 780
 Db 780 SPMTATVAVNNFLVYSSLSPTKAGPKIVSHLALVDNKSLENIENNDYIKHOPEISL 839
 Qy 781 SPLKAINSPNIFLYVSSHSSSKAPVSHLQLOVDEKSLNMSNENDEYKHLHPOTFL 840
 Db 840 QNOLRLGIMQICPOAYFSVMSHLLVALKAVQSNVTVAGSFVQLQGTTLTGALN 899
 Qy 841 WFOVRGLMIVSPESFSEFSEHLRLALFAEENVTWBCSEFLLQFLRGRTFLRVLN 900
 Db 900 LQYFDDPESELSTLRSTHPIIRGNKTSPPRAHSVLETCDSQVPTIQQDYVSAFEPNNE 959
 Qy 901 LEYFMDPESELSTLRKAVSINGNKMSVYDVS-FKTYFENLQPAINDETSNAFENYSE 959
 Db 960 WERILAKEDENKVSYDMOMRASPDLSGTGWMKLSPROXYRIPCLEVDVNDIVVQDMLEI 1019
 Qy 960 WRNMFADDEETIINYNINIPRALPDISGTYWLSPKCKIPKLEVQVNMGRADALLQV 1019
 Db 1020 LMTFVSASQIETLHNSGPTESIRPALLESKASVTKSISKLELSAADELLTLP 1079
 Qy 1080 ESLEVSQTIQSDQIFPNLDKFLCLKELSYDLGENINVFYIPEEPFNHMEKLLIQIS 1139
 Db 1080 QSLVESSETNQLPDLFPHLHKFLGKELCYRLDGKPRVLSVLEEFELNHNMEKLSIRTS 1139
 Qy 1140 AEYDPSKLVKLQNSPNLHVPHLCNFPDPSGLMTVLVSCCKLTKETSDSFQAVPFLV 1199
 Db 1140 YESDLSKLVKFLQNPPLHVPHLCNFPDPSGLMTVLVSCCKLTKETSDSFQAVPFLV 1199
 Qy 1200 ASLPNFIKLTLNLEGOFPDEETSEKFAVILGSLNLEELIPTDGGYVRAKILIQOC 1259
 Db 1200 NILPNFVSLKLSLKGQGFADKETSEKFAQALGSLRNLELLVPTGCGDGHQAKLIVQOC 1259
 Qy 1260 QOLHCLVLSFEFTLANDSVYELAKVAISGGFQKLENLKLSINHTITEGYRNPFQALDN 1319
 Db 1260 LQPLCLVLAFLHILDESVYELIG-AATSGSFQKLENLKLSINHTITEGYRNPFQALDN 1319
 Qy 1320 MPNLQEDISRHFTETCIKQATTVKSLSCVLRPLRLNMLNSWLDADADIALNLMKE 1379
 Db 1319 LPNLQMLNLCRNIPGIVQATTVKALCHCVSRPLSRLRLMLSWLDEDEMKYINQVKE 1378
 Qy 1380 RHPOSRYTLITLQKMLPSPPII 1401
 Db 1379 RHPOSRYTLITLQKMLPSPPIV 1400

RESULT 7
 CARC_HUMAN

ID CARC_HUMAN STANDARD: PRT; 1024 AA.
 AC OSNP4; 096J83; 096J82; 096J81;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Caspase recruitment domain protein 12 (ice-protease activating factor)
 DE (Ipadf) (CARD, LRR, and NACHT-containing protein) (Cian protein).
 GN CARD12 OR CIAN1 OR CIAN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=21268963; PubMed=11374873; Lavellee M., Manj G.A., Brown M.,
 RA Geddes B.J., Wang L., Huang W.-J.,
 RA Jurman M., Cao J., Morgenstern J., Merriam S., Glucksmann M.A.,
 RA Distefano P.S., Berlin J.;
 RT "Human CARD12 is a novel CED4/Apaf-1 family member that induces
 apoptosis.";
 RT Blochem. Biophys. Res. Commun. 284:77-82(2001).
 RL [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
 RX TISSUE=Lung;
 RC PubMed=11472070;
 RA Damiano J.S., Stehlik C., Plo F., Godzik A., Reed J.C.;
 RT "CLAN, a novel human CED-4-like gene.";
 RL Genomics 75:77-83(2001).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Leukocyte;
 RX PubMed=11390368;
 RA Poyet J.-L., Srinivasula S.M., Tranl M., Razmara M.,
 RA Fernandes-Alnemri T., Alnemri E.S.;
 RT "Identification of Ipadf, a human caspase-1-activating protein related
 to Apaf-1.";
 RL J. Biol. Chem. 276:28309-28313(2001).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Gingras M., Olu J., Margolin J.F.;
 RT "Differential expression of the caspase recruitment domain protein 12
 (CARD12) during monocytic differentiation.";
 RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 586-1024 FROM N.A. (ISOFORM 1).
 RA Auffrey C., Ansgore W., Balabio A., Estivill X., Gibson K.,
 RA Leinrich H., Pouska A., Lundeberg J.;
 RL Submitted (Jul-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Plays a role in the promotion of apoptosis.
 CC -1- SUBUNIT: Self-associates and binds to ASC, pro-caspase-1, Nod2,
 CC Bcl10 and NALP1 (NAC) by CARD-CARD interaction.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic filaments.
 CC -1- ALTERNATIVE PRODUCTS: 4 isoforms, 1/CLAN (shown here), 2/CLAN,
 CC 3/CLAN and 4/CLAN; are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Isoform 2 is expressed ubiquitously, although
 CC highly expressed in lung and spleen. Isoform 1 is highly expressed
 CC in lung, followed by leukocytes especially monocytes, lymph node,
 CC colon, brain, prostate, placenta, spleen, bone marrow and fetal
 CC liver. Isoform 4 is only detected in brain.
 CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 NACHT DOMAIN.
 CC -1- SIMILARITY: CONTAINS 14 LEUCINE-RICH REPEATS (LRR).
 CC -----
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 CC -----
 CC EMBL; AY032589; AAK38730.1; -
 DR EMBL; AY027787; AAK14776.1; -

DR EMBL; AY027788; AAK14777.1; -
 DR EMBL; AY027789; AAK14778.1; -
 DR EMBL; AY027790; AAK14779.1; -
 DR EMBL; AY035391; AAK59843.1; -
 DR EMBL; AF376061; AAK53443.1; -
 DR EMBL; AL38934; CAB97523.1; -
 DR PROSITE; PS50209; CARD. 1.
 DR PROSITE; PS50837; NACHT. 1.
 KW Apoptosis; App-binding; Repeat; Leucine-rich repeat;
 KW Alternative splicing.
 FT DOMAIN 1
 FT NP_BIND 163 476
 FT REPEAT 169 176
 FT REPEAT 7 30
 FT REPEAT 258 281
 FT REPEAT 578 598
 FT REPEAT 656 679
 FT REPEAT 735 758
 FT REPEAT 762 785
 FT REPEAT 787 812
 FT REPEAT 824 847
 FT REPEAT 848 870
 FT REPEAT 878 902
 FT REPEAT 911 933
 FT REPEAT 936 963
 FT REPEAT 965 985
 FT REPEAT 999 1021
 FT VARSPLIC 89 753
 FT VARSPLIC 155 156
 FT VARSPLIC 157 1024
 FT VARSPLIC 90 92
 FT VARSPLIC 93 1024
 FT CONFLICT 138 138
 FT CONFLICT 393 393
 FT CONFLICT 420 420
 FT CONFLICT 678 678
 FT CONFLICT 678 678
 SQ SEQUENCE 1024 AA; 116158 MW; 49378DBB54938E0F CRC64;

Query Match 8.9%; Score 654; DB 1; Length 1024;
 Best Local Similarity 23.7%; Pred. No. 3.5e-31;
 Matches 263; Conservative 197; Mismatches 410; Indels 238; Gaps 42;
 QY 344 FLONKRS-SAEVTPDLOSRCGELCELETSESNEEDSIAPVPIYEMAGOEAFOWFOEAKN 402
 DB 69 FLKSLKEMNYPLPQDLNQ-----SLFHTSGEDLD----- 100
 QY 403 LNEQLRAAYTSAPFRHMSLIDTSSDLARDHLGCDLSI---ASKHISKPV----- 449
 DB 101 LAQDLKDYHPSFLNF-----YPLGEDIDITFNLKSTFEPVLMRKQDHNHR 148
 QY 450 QEPVLVPEVFGNLSVMVCEGEGAGSGKTVLAKIKFIWASGCCPLNPFOLVFTYLSST 509
 DB 149 VEQLTLNLALALOSPCTIEEGSGKSTLQRIAMLMGSGCKALTKFKVFFLRIS-- 206
 QY 510 RPDEGLASICDOLLKEKGSVTEMCMRNIIOLKQGVFLLDYKEISIPQ---VIGKL 566
 DB 207 RAQGLGFLTEQLDQDLIDIGTIRKQFFAMLMKLRVFLFDGYNEF--KQNCNEIGAL 264
 QY 567 IOKNLSFTCLLIIVRTNRARDIRYLETIEIKAPRYNTVCILKFSHNRFLRKM 626
 DB 265 IKENHREFNMVIVTPTTECLRIHROFGALTAEGDWTEDSAQALREVILIKELA--EGIL 322
 QY 627 VYFGNOSLOKIKRPLVAALICAMRPQYPRPSPDDVAVRSYMERLSLNK-----A 680
 DB 323 LQIQSKRLRLMKTPLELVITCALQMGSEPHSTQTTLEHTFEDLLIQKHKRHKGA 382
 QY 681 TAEILKATVSSCGELATLGFSCCFEFDNDLAEAGVDEDELTWCLMSKFTAORLPFY 740
 DB 383 ASDFLR-SLDKGDALGCVSHKRFELQDY--SSVNEVDVLTGTGLCKTAQGRFKY 439
 QY 741 RFLSPAQEFPLAGMRLLIELLSDROHODGLYHLKQINSPMATVSAVNNFLNTV--SSL 798

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Db 440 KFFHKSQEVYACGRSLSLTSHPEEYTKGCVLQKNVSIIDITSTYSSILRTCCSSV 499
Qy 799 PSTKAGPKIVSHLLHLYDN-----KESLESENDDVTLKHQPELSIQMOL 843
Db 500 EATRA---VVKHLAAVYQIGCLLSIAKRPLMRQESLSQVKN-----TTEQEI 545
Qy 844 LRLLMCIQONFVSNVSEHLVLAUKTAYQSNF--VAACSPVYQILOGRTLTGALNTL-Q 901
Db 546 LKAI-----NINSEVCGIHL-----YQSTSKSLSDGEFAFPQKSLYINSGNIPD 593
Qy 902 YFFDHPESLSILSRTHIFPIRGNKTSPPRAHPSVLETCPDKSQVPTIDQYASAFEPDME 961
Db 594 YLFD-----FEHLPPNC--ASALDFIKLDFYGG--AASME 625
Qy 962 RNLAKEEDNVKASYMDQRRASPDLSTGYWKLSPKQYKIP-----CLEYDV 1006
Db 626 -----KAEDTGGIHMEEAFETY-IPSRVSLTFPMKQEFRTLEVTL 666
Qy 1007 NDIVNGQDMELIMTVFSASQRIEHLNHSRGFTESIRPALELSKASVTGCSISKLELS 1066
Db 667 RDSRLKKKODIRYLKIFSSATSLRLQIKRCGAVAGSISLVLSCK-NIYSLVMSPLR 725
Qy 1067 AADQELLTLPSLESLVSGTIGSODQIFPN--LDKFLCKELSVDEGNINFEVPIPEE 1124
Db 726 IEERRHITSVTNLKLSIH---DIQNRLPGLTDSLGINKLNLKLMNDIKM----- 775
Qy 1125 FPFHHEKLLTQISAEVDPKVLKILQNSPFLHVFHLKCNFSDGSLMTMLVS----- 1179
Db 776 -----NEEDDAIKLAEGLKNLKKMCLFHL--THLSDDGEMDMYVLSLSE 818
Qy 1180 -CKKLTFRFSDSEF--GAVPFVA-SLPNFSILKILNLEGOQFPDETSKRYAVILGSLIS 1235
Db 819 PC-DLEETQVSCCLSANAVAKIILQNLNMLVKSILDL--SEVYLEKQGEALHELIDMAN 876
Qy 1236 NLEE---LILPTGDIIRVAKLIQCCOOLHCLRVLSFEKTLNDQSVVKAISGCF- 1291
Db 877 VLEDTLALMPKCDVQGSLSLKLHLEVPOLVYKLGKLNMRUDT-----EIRILDAF 931
Qy 1292 -----OKLEMLKLSINHKITEEGYRNFQALDNNMNIQDELDIRHTECIRKATYKSL 146
Db 932 CKNPPLKFPDQNLAGN-RVSSDGLAFMGVFNENLQVLFDFSS---TKFELPPALVRKL 987
Qy 1447 SCQVLRPLRLIRLNMLSMLLDADIDALL 1374
Db 988 SOVLSKLTFLQBARLYVGMQFDDDLSTV 1015

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RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertton-Horvat G.,
RA Farahani R., McLean M., Ikeda J., Mackenzie A., Koreljak R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
RT family of IAP genes."
RL Nature 379:345-353(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RL receptor-associated factors."
RN Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RP [4]
RP STRUCTURE BY NMR OF 266-363.
RX MEDLINE=99332054; PubMed=10404221;
RA Hinds M.G., Norton R.S., Vaux D.L., Day C.L.;
RT "Solution structure of a baculoviral inhibitor of apoptosis (IAP)
RT repeat."
RL Nat. Struct. Biol. 6:648-651(1999).
CC -I- FUNCTION: APOPTOTIC SUPPRESSOR. THE IAP MOTIFS REGION INTERACTS
CC WITH THE RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (potentl.).
CC -I- TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.
CC MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY,
CC AND PANCREAS. LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD
CC LEUKOCYTES.
CC -I- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -I- SIMILARITY: CONTAINS 3 IAP REPEATS.
CC -I- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -I- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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DR EMBL; I49431; AAC41942.1; -
DR EMBL; U45879; AAC50372.1; -
DR EMBL; U37547; AAC50508.1; -
DR PDB; 1OBH; 20-OCT-99.
DR MIM; 601721; -
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_fing.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS00518; zf_RING_1; FALSE_NEG.
DR PROSITE; PS00089; zf_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat; 3D-structure.
FT REPEAT 46 113
FT REPEAT 184 250
FT REPEAT 269 336
FT REPEAT 453 543
FT ZN_DOMAIN 571 606
FT ZN_FING 571 606
FT CARD 157 157
FT CONFLICT 308 308
FT CONFLICT 414 414
FT CONFLICT 514 514
FT CONFLICT 514 514
SO SEQUENCE 618 AA; 69899 MW; C1778D328063586D CRC64;

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Query Match          6.3%; Score 462; DB 1; Length 618;
Best Local Similarity 26.0%; Pred. No. 4.2e-20;
Matches 155; Conservative 82; Mismatches 214; Indels 146; Gaps 22;

QY 38 LEEEOKEFRAMOKGYNSQMSSEAKRLKTFVTEPYESWIP---QEMAAAGFYTVKSG 94
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 28 LSDMTNSKKQMKKDFDSE-----LYRMSTYTFPPAGVPYSESLARAGFYTVGVNDK 80
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 95 IQCFCCSLLIFGAGITRLPIEDHKRFHPDCGF---LNNKDVGNIAKYDIRVKN----- 144
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 81 VKCFCCGIMLDMNKLGSDPIOKHKOLYPCSFIONLVASLSGSTSKSPMNSPAHSLS 140
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 145 -----LKSRL-----RGCKMRY---QEERARLASFPNPFYVOG 175
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 141 PTLHSISLFGSSYSLSNPLNSRAVEDISSRINPYISIAMSTEARLTYHMP--LTF 198
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 176 ISPCVLSAGFVFTGKODTVOCFSCGCGCLGNMEGDDPWKEHAKWFPCEFLRSKSSSE 235
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 199 LSPSELARAGFYITGPGDRVACFACGCKLSMWEKDDAMSEHRRHFPNCPFL---ENSL 255
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 236 ITQYIOSYKGFVDITGEHFVNSWQRELPMASAYCNDISIFAYEELRDSFKDMPRESAVG 295
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 256 TLRFESIS-----NLSMOT-----HAARMRTFMYWPFSSVPEQ 286
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 296 VAALAKAGLEFYTKIDYQCFSCGCGCLEKNOEGDDPLDHRPCNCFPLQMKSSAEVT 355
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 287 PEQLASAGFYTVGRNDVKCFCCDGLCWESGDDPWVHAHWPFCETLLRMKQO-EFV 345
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 356 PDLOS-R-GELELETTESNLEDSIAVGPVPEMAQGEAOFQAKNLEOLRAAYTSA 414
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 346 DEIGRYPHLEQLISTSDTJGEEN--ADPPIHFGPGESS--SEDAVMNTPVVASALEM 402
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 415 SFRHSLDISSDATDHLGLGDSIASKHLSKPVQEP-LVLPVEFGLNSVYCVGEENG 473
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 403 GFNR-----DL-----VKQVQSKILTFGENYKTVINDIVSALLNAE 438
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 474 SGKTYLTK-KIAFLMASGCCPLNRFOLVFLYSLSTRPDESLAITCDLLEKGSYTE 532
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 439 DEKREEEKQAEEMASDLSIRKRNALFOQLTCVLP-----ILDNLK----- 484
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 533 MCMRNIIQOLKNQVFLLDYKEICISPOVIGKLIQKNHLSRTCLLIARTRNRARDI 589
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 485 ---ANVINKQEHDI-----KQKTOIFLQARELID-----TILVKGNAANI 523
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
BIR3_MOUSE
ID BIR3_MOUSE STANDARD: PRT; 612 AA.
AC 062210; 008864;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis
  protein 2) (MIAP2) (MIAP-2).
DE BIR3 OR API2 OR IAP2.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE=96128127; PubMed=6548810;
RA Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-Traf signaling complex contains two novel proteins related
  to baculoviral inhibitor of apoptosis proteins."
RL Cell 83:1243-1252(1995).
RP
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98110590; PubMed=9441758;
RA Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;

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RT "Genomic characterization of the mouse inhibitor of apoptosis protein
  1 and 2 genes."
RL Genomics 46:495-503(1997).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF HETEROMER ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (potentially).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, SPLEEN, LUNG,
CC LIVER, SKELETAL MUSCLE, KIDNEY, AND TESTIS.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC
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CC
DR EMBL; L49433; AAC42078.1; -
DR EMBL; U88909; AAC53532.1; -
DR HSSP; Q13490; 10BH.
DR MGP; MGI:1197009; BIRC3.
DR InterPro; IPR001370; BIR.
DR InterPro; IPR001315; CARD.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; Zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS01443; BIR_REPEAT_2; 3.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Apoptosis; Zinc-finger; Repeat.
FT REPEAT 177 243 BIR 1.
FT REPEAT 262 329 BIR 2.
FT REPEAT 447 537 BIR 3.
FT DOMAIN 447 537 CARD-TYPE.
FT ZN_FING 565 600 RING-TYPE.
FT CONFLICT 380 380 E -> K (IN REF. 2).
SQ SEQUENCE 612 AA; 69676 MW; E08969D93C6C610D CRC64;

Query Match          6.3%; Score 457.5; DB 1; Length 612;
Best Local Similarity 26.6%; Pred. No. 7.7e-20;
Matches 148; Conservative 73; Mismatches 207; Indels 129; Gaps 19;

QY 43 OKERAKMOKG---YNSQMSSEAK-----RLKTFVTEPYESWIP---QEMAAAGFYTV 89
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 16 QKLRIMKEKSTLISMTWTKSEKMKFDFSCELYRSTYSAPFRGVPVSERSLARAGFYTV 75
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 90 GYKSGIOCFCCSLLIFGAGITRLPIEDHKRFHPDCGF---LNNKDVGNIAKYDIRVKNL 146
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 76 GYNDKVKCFCCGIMLDMNKQGDSPVEKHQFPSPCSFYQTLTSLASLQSSK---NMSPVK 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 147 SRL-----RGK-----KMRQOEERARLASFRNPFYVO 174
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 133 SFRHSSPLERGGISNLCSSPLNSRAVEDFSSRMDPCSYAMSTEARLTYSMMP--LS 190
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 175 GISPCVLSAGFVFTGKODTVOCFSCGCGCLGNMEGDDPWKEHAKWFPCEFLRSKSSSE 234
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 191 FLSPSELARAGFYITGPGDRVACFACGCKLSMWEKDDAMSEHRRHFPNCPLENTSETQ 250
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 235 EITQYIOSYKGFVDITGEHFVNSWQRELPMASAYCNDISIFAYEELRDSFKDMPRESAV 294
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 251 RES-----ISNLSMOTHSAARLRTFLYNPSPVPV 278
Oy 295 GVALAKAGLFTYGIKIDVOCFSCGGLKEMOBDPLDHTPCFPCFLOMKSASAEV 354
Db 279 OPEOLASAGFTYVNDVRCFCDCGLRCMCPDPMLEHAKWPRCFELRMKGQ-EF 337
Oy 355 TPDLQSR-GEICELLETTESNEDSIAGPIYPEMAOGEAOWFOEARNLNEOLRAVTS 413
Db 338 VDEIQARYPHLLRLSTSDTPGEENADPTETVYHFGPE-----SS 379
Oy 414 ASFRHNSLIDISDLTDHLLGCDLSIAKHSKBPVOPVLYPEVFGNLSVMCV-----E 469
Db 380 EDVYWMSTPVYKALE-----WGRSRSLVQOTVOROI---LATGKNYVNDIVSVLMAE 432
Oy 470 GEAGSGKTYVLKKAFLAMAGCCPLNRFOLYFVLSSTSPDGLASITCDLLEKES 529
Db 433 DEEREERK---ERQTEENASGDLILIRKNMALFOOLTHVLP-----ILDNLL-EAS 480
Oy 530 VTEMCRNITIOOLKNQV 546
Db 481 VITKQEHDIRO-KTOI 496

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RESULT 10
BIR2_MOUSE
AC 008863; STANDARD; PRT: 600 AA.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Baculoviral IAP repeat-containing protein 1 (MARP1) (MARP-1).
OS BIR2 OR API1 OR IAP1.
SN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98110590; PubMed=9441758;
RA Lister P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT Genomic characterization of the mouse inhibitor of apoptosis protein
RT 1 and 2 genes.
RL Genomics 46:495-503(1997).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH THE RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC or send an email to license@isb-sib.ch).
DR EMBL: U68908; AAC53531.1;
DR HSRP: Q13490; IOBH.
DR MGD: MGI:1197007; Birc2.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_Ling.
DR Pfam: PF00653; BIR_3.
DR Pfam: PF00619; CARD_1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.

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DR SMART; SM00114; CARD; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS00518; zf_RING_1; FALSE_NEG.
DR PROSITE; PS50089; zf_RING_2; 1.
DR Apoptosis; zinc_finger; Repeat.
FT REPEAT 27 94 BIR 1.
FT REPEAT 167 233 BIR 2.
FT REPEAT 253 320 BIR 3.
FT DOMAIN 436 525 CARD.
FT ZN_FING 553 588 CARD.
SO SEQUENCE 600 AA; 67198 MW; ADVF73E6849317D1 CRC64;

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Query Match
Best Local Similarity 6.0%; Score 440; DB 1; Length 600;
Matches 145; Conservative 88; Mismatches 226; Indels 162; Gaps 19;

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Oy 47 AKMOKCYNS-----QMRSEAKRLKTFVYEPYSSWIP---QEMAAQFTYGVKSGIOCF 98
Db 9 AKLMKSADTFELKYDFSCELYRLS---TYSAPPPGVPSERSIARAGFYTYTGANDVKCF 65
Oy 99 CCSLILFAGLRLPIEDHKRPHPCGCLLNKDVGNIAKYDIRKYNLSRLRGKMY-- 156
Db 66 CCGMLDMNKKODSPMEKHKRLYPCNFVOTLNPANSLASPPSLPSTMASTMPLEFNS 125
Oy 157 -----QEEARLASRRNMPFYOGTS 177
Db 126 SENTYFSGSYSPSPDPVFNFRANQDCPALSTSPYRPAKNTTEKARLLTYETNP--LSFLS 183
Oy 178 PCVLSAAGFVFTGKODTVOCFSCGGLKEMOBDPLDHTPCFPCFLOMKSASAEVTP 356
Db 184 PAKLAKAGFYIIGPDVYACFACDGKLSMWERKDDAMSEHSHRPPSCFPLDLOQS----- 239
Oy 238 QYISYKGFVDITIGEHFVNSWVORELPMASAYCNDSI-FAYELRLDSFKWPRSAVGV 296
Db 240 -----ASRYTVNLSMORHAARIRTFESWMPSSALVHS 271
Oy 297 ALAKAGLFTYGIKIDVOCFSCGGLKEMOBDPLDHTPCFPCFLOMKSASAEVTP 356
Db 272 QELASAGFYTYGSHSDVRCFCDCGLRCMCPDPMLEHAKWPRCFELRMKGQ-EF 337
Oy 357 DLQSR-GEICELLETTESNEDSIAGPIY-PEMAOGEAOWFOEARNLNEOLRAVTS 413
Db 332 VQAGVPHLLRLSTSDSP-EDENADAIVHFGESSEDEVYMSSTPVYKALEMGFSRS 390
Oy 401 ---KLNLEQLRAA---YTSASFHMSLIDISSDL-----ATDHLGCDLSIAKHSK 447
Db 391 LVROTVORQIATGENTYVSDIYIGLLDAEDDEREQMQLAEESDILLIRKNKV 450
Oy 448 PVQE-PLVLPVEFGNLSVMCVGEAGSGKTYVLKKAFLAMAGCCPLNRFOLYFVLSL 506
Db 451 LEQHLTCVTPMLYCLLARAITDEECNAVK----- 480
Oy 507 SSTPRDGLASITCDLLEKESVTEMCRNITIOOLKNQV---LELDDYK-----EICS 558
Db 481 --QKPHLOASTLIDVYLAK-GNTAATSPRNSLRREIDPALYNDIVQODIRSLPTDIAA 537
Oy 559 IP--QVIGKLIQKNSLRCL 577
Db 538 LPMEQLRLK-QEERCKKCYCM 557

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RESULT 11
BIR2_HUMAN
AC 013489; Q16628; Q9UP46; STANDARD; PRT: 604 AA.
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Baculoviral IAP repeat-containing protein 1 (Inhibitor of apoptosis

```

DE protein 1) (HAP1) (HAP-1) (C-IAP2) (TNFR2-TRAF signaling complex
 DE protein 1) (IAP homolog C).
 GN BIRC2 OR API1 OR IAP1 OR MHC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 ON NCBI_TaxId=9606;
 RX MEDLINE=96128127; PubMed=8548810;
 RA Roche M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
 RT "The TNFR2-TRAF signaling complex contains two novel proteins related
 RT to baculoviral inhibitor of apoptosis proteins.";
 RL Cell 83:1243-1252(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=96149249; PubMed=8552191;
 RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertnon-Horvat G.,
 RA Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
 RT "Suppression of apoptosis in mammalian cells by NAIP and a related
 RT family of IAP genes.";
 RL Nature 379:349-353(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal Liver;
 RX MEDLINE=96209843; PubMed=8643514;
 RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
 RT "Cloning and expression of apoptosis inhibitory protein homologs that
 RT function to inhibit apoptosis and/or bind tumor necrosis factor
 RT receptor-associated factors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99252096; PubMed=10233894;
 RA Horrevoets A.J., Fontijn R.D., van Zonneveld A.J., de Vries C.J.,
 RA ten Cate J.W., Pannekoek H.;
 RT "Vascular endothelial genes that are responsive to tumor necrosis
 RT factor-alpha in vitro are expressed in atherosclerotic lesions,
 RT including inhibitor of apoptosis protein-1, stannin, and two novel
 RT genes.";
 RL Blood 93:3418-3431(1999).
 CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
 CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
 CC FORM AN HEMEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
 CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (potential).
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FETAL LUNG, AND KIDNEY. IN
 CC THE ADULT, EXPRESSION IS MAINLY SEEN IN LYMPHOID TISSUES,
 CC INCLUDING SPLEEN, THYMUS AND PERIPHERAL BLOOD LYMPHOCYTES.
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: LA9432; AAC41943.1;
 DR EMBL: U45878; AAC50371.1;
 DR EMBL: U37546; AAC50507.1;
 DR EMBL: AF070674; AAC83232.1;
 DR HSSP: Q13490; 1QBH.
 DR MIM: 601172;
 DR InterPro: IPR001370; BIR.
 DR InterPro: IPR001315; CARD.
 DR InterPro: IPR001841; znf_fing.
 DR Pfam: PF00653; BIR; 3.

DR Pfam: PF00619; CARD; 1.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00238; BIR; 3.
 DR SMART: SM00114; CARD; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS01282; BIR_REPEAT_1; 3.
 DR PROSITE: PS50143; BIR_REPEAT_2; 3.
 DR PROSITE: PS50209; CARD; 1.
 DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KW Apoptosis; Zinc-finger; Repeat.
 FT REPEAT 29
 FT REPEAT 169
 FT REPEAT 255
 FT REPEAT 439
 FT DOMAIN 557
 FT ZN_FING 592
 FT CONFLICT 18
 FT CONFLICT 119
 FT CONFLICT 153
 FT CONFLICT 163
 FT CONFLICT 165
 FT CONFLICT 191
 FT CONFLICT 364
 FT CONFLICT 552
 FT SEQUENCE 604 AA; 68371 MW; 8581A0B8A9ABA47 CRC64;
 Query Match 6.0%; Score 436.5; DB 1; Length 604;
 Best Local Similarity 24.5%; Pred. No. 1.3e-18;
 Matches 147; Conservative 84; Mismatches 200; Indels 169; Gaps 22;
 QY 69 TYPEPSSNIP---QEMAAAGFTFGYKSGICGFCSSLLTFAGLTRLPIEDHKRHPGCG 125
 DB 35 TYSTFPAGVPVSEKSLAAGFYTGVDKVCFCGGLMLDMKKRGDSPTKHKRLYPSCR 94
 QY 126 FLIN-KDQGN-----AKYDTRVKLKLKSLRGK----- 153
 DB 95 FVQSLNSVNNLEATSQPFPPSSVYNSTHSLRGTENSGYFPGSYNSNSPNVSNANDF 154
 QY 154 ---NR-----YQEBEARLAFSRMPPFYVQGISPCVSEAGFVTGKODTYQCRSGCGL 204
 DB 155 SALMKSSYHCAMNNENALTFQTPW--LTFSLSPDLAKAGFYIYIGPDRVACFACGCKL 212
 QY 205 GNMVEGDDPMKHKWPKCFELSKSKSEETIOTIOSYKGFVDITGHEFVNSWQRELCP 264
 DB 213 SNMEPKDANSEHLRHPKCPFIEMQ--LQDSRTTVS-----NLS 251
 QY 265 MASATCNDSTIFAYEELRLDSFKDMPRESAVGVAALAKAGLFYTGIKDIVOCFSGGCKLEK 324
 DB 252 MOT-----HAARKTFEPMPSVLYNPEDLASAGFYIYVGSNDYKCFCCDGGJRC 301
 QY 325 WQGGDPLDDHTRCFPNCPFLQNMKSSAEVTPDIQSGKELCELLTETSES----- 374
 DB 302 WESGDDPMVQAKMFRPCEYLIRIGQEFIRQVQASYPHLLLEQLLSTDSGDENAESSI 361
 QY 375 -----NLDSIAVG--PIVEMAGQEAQMPQAKNLEOLBRAVTSASRHHSLDIS 425
 DB 362 IHPEGDEHSDALIMNTPV--NAAVEMGFSRLSVKOTVORKILATENR-----LV 413
 QY 426 SDLATDHLGCDLSTASKHSKPVQEPVLVPEVFNLSVWCVEGASGCTVLLKRIAF 485
 DB 414 NDLYVID-LINAEDELREERERATE-----EKSNOLLILRK-- 449
 QY 486 LMASGCCPLNRFOLVFLYLSSTRPDEGL-ASIIQDQ-----LLEK- 526
 DB 450 -----NRMALFQHLTCVPIPLDSILTLVAGIINEQEHVIRKOTQSLQARELLIPTI 499
 QY 527 --EGSVTECMKRNIIQOK---NOVLFLDDPYK-----EISIPQVTKLQKHLNSTPC 576
 DB 500 LVGNIAATVFRNSLQEAEAVALYELHFLVQODIKIPTYTEDVSDLP--VEQLRLQDEKTC 557
 RESULT 12

BIR4_MOUSE
ID BIR4_MOUSE STANDARD: PRT: 496 AA.
AC 060989: 008865;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP homolog A) (MIAP3) (MIAP-3).
GN BIR4 OR API3 OR XIAP OR AIP4 OR MIRA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6 X CBA; TISSUE=Liver;
RX MEDLINE=96209843; PubMed=8643514;
RA Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors";
RT Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Farahani R., Lefebvre C., Korneluk R.G., Mackenzie A.E.;
RT Submitted (JUN-1997) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. INHIBITOR OF CASPASE-3 AND CASPASE-7 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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DR EMBL: U36842; AAC52594.1; -
DR EMBL: U88990; AAB58376.1; -
DR HSSP: Q13490; 10BH.
DR MGD: MGI:107572; Birc4.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; ZnF_fing.
DR Pfam: PF00653; BIR_3.
DR SMART: SM00238; BIR_3.
DR SMART: SM00184; RING_1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NCG.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 26 93 BIR 1.
FT REPEAT 163 230 BIR 2.
FT REPEAT 264 329 BIR 3.
FT ZN_FING 449 484 RING-TYPE.
FT CONFLICT 208 208 E -> K (IN REF. 2).
FT CONFLICT 317 317 E -> D (IN REF. 2).
FT CONFLICT 322 322 W -> C (IN REF. 2).
FT CONFLICT 346 346 S -> P (IN REF. 2).
FT CONFLICT 360 360 S -> P (IN REF. 2).
FT CONFLICT 388 388 I -> L (IN REF. 2).
FT CONFLICT 449 449 C -> S (IN REF. 2).
FT CONFLICT 462 462 V -> F (IN REF. 2).
FT CONFLICT 468 468 V -> A (IN REF. 2).
FT CONFLICT 490 490 K -> N (IN REF. 2).
SQ SEQUENCE 496 AA: 56079 MW: EC5FAE07999F2CDD8 CRC64:

Query Match 5.9%; Score 431.5; DB 1; Length 496;
Best Local Similarity 28.8%; Pred. No. 2e-18;
Matches 121; Conservative 57; Mismatches 163; Indels 79; Gaps 12;
QY 60 EAKRKTPTVYEPSSNPDEMAAGFYFTGVSGIOCFCCSILPGAGLTRLPED---- 116
DB 26 EFNRLKPTANPSSSPVASTLARAGFLYEGEDDVQCFSC-----AIDRQVGSAY 80
QY 117 --HFRFDPDC---GFLINDVGNIAKYDIRVANKSR----- 148
DB 81 GRHRIRISPNCFINGFYFENGAGQSTNPGLNQYSENCVGNRPFADRPETHADYL 140
QY 149 LRGKMM-----RQEEANLASFRRMFPFYVGISPCVLSSEAGFYFTGRDPVVO 196
DB 141 LRTQGVYDIDDTYPRNPANCSEARLKSFQWNPDYAH-LTRRELASQVLYTGADDDVQ 199
QY 197 GFSCGCGCLNMERGDDPWKEHAKWPKCEFLSKSSSEITQYIYSGVYDITGEHFN 256
DB 200 CFCCGCGKLEWMEPCDRAWESEHRHPNCFVYGRN-----VNVSESGVS 244
QY 257 SWQRELPMASAVCNDSIFATYELRLDSFKDNPRESAVGVALAKAGLYTGIDVOCF 316
DB 245 S--DRNFPNSTSPNPPAMAEYEARTVETGW--TSSVYKQLARAGFYALGEGDKYCF 300
QY 317 SCGGCLEKKQESDDPLDHTTRCFNCPFLQNMKSSAEVTPDLSRGELLETTSF--- 373
DB 301 HCGGGLTMRKPSDEWEOHAKWPGCKYLLDEKQ-EYINNIHLTSLSELSGTAKTP 359
QY 374 ---SNLEDSIAVGPIVPMAGGEQWQEAANLEQI:PAVTSFRRMSILDISSDLAT 430
DB 360 SLTKRIDDTIQNPRVQALIMGFSEFDIKTKMEKIQTSGSS---YLSLEVLIADLV 415
RESULT 13
BIR4_RAT
ID BIR4_RAT STANDARD: PRT: 496 AA.
AC 099016;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
DE (IAP homolog A) (RIAP3) (RIAP-3).
GN BIR4 OR API3 OR XIAP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Salto N.;
RT "Rattus norvegicus X-linked inhibitor of apoptosis (riap3) mRNA";
RT Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. INHIBITOR OF CASPASE-3 AND CASPASE-7 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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DR EMBL: AB033366; BAA85504.1; -
DR HSSP: Q13490; 10BH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; ZnF_fing.

DR Pfam; PF00653; BIR. 3.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00238; BIR. 3.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS01282; BIR_REPEAT_1; 3.
 DR PROSITE; PS0143; BIR_REPEAT_2; 3.
 DR PROSITE; PS00518; zf_RING_1; FALSE_NEG.
 DR PROSITE; PS00089; zf_RING_2; 1.
 KW Apoptosis; zinc-finger; Repeat.
 FT REPEAT 26 93 BIR 1.
 FT REPEAT 163 230 BIR 2.
 FT REPEAT 264 329 BIR 3.
 FT ZN_FING 449 484 RING-TYPE.
 SO SEQUENCE 496 AA; 56072 MW; E250E3C77461A469 CRC64;

Query Match 5.7%; Score 416.5; DB 1; Length 496;
 Best Local Similarity 28.3%; Pred. No. 1.5e-17;
 Matches 119; Conservative 60; Mismatches 162; Indels 79; Gaps 12;

QY 60 EAKRLKFTVTEPYSSWIPQMAAGFYFTGKSGICFCSCSLIFGAGLTRLPED--- 116
 DB 26 EFNRLKFTFANPPSSPVASLTLARAGFLYTGEGDTRCFSCS-----AAVDRMVGDSAV 80
 QY 117 --HRRFHDGCF-----LNRKVGNIKAYD 139
 DB 81 GRHRISPNCRFINGFYFENGATOSTSGIONGQYKSCNCGNNHFPALDRPSETHADYL 140
 QY 140 IR---VNNLSRLRGKMRROEEBARLASFRNPFYVQGISPCVLSRAGFYFTKQDTVQ 196
 DB 141 LRTQVVDISPTIYPRNPAMCSEARLKTQFNWPDYAH-LSPRELASGLTYTIDQVQ 199
 QY 197 CFSCGGGLGKNEEDDDPMKEHAKWPKCEFLRSKSSSELTQYLSQKGFIDINGEHNV 256
 DB 200 CFCCGGGLKMKNEPCDRAHSEHRRHPNCFEVLGRN-----VNVSESGVS 244
 QY 257 SWVQRELPMASAYCNDISFAYEELRLDSFKDMPRESAVGAALAKAGLFYTGIRDIYOCF 316
 DB 245 S--DRNPNSTNSPRNPAMAEYDARIYVFGTW--LYSVNKGQLARAGFYALGEGDKVCF 300
 QY 317 SCGCGLEKMGEGDPLDDHTRCFPNCPFLQNMKSSAEVTPDQSRGELCELTTSE--- 373
 DB 301 HCGGGLTDMKSEBDPMEDHAKWPGCYKYLDEKCO-EVINNIHRTHSIGESVPTAEKTP 359
 QY 374 ---SNLSDSLAVGPIYVEMAGSEAGQPEAKNLNQLRAATVSFRHMSLDDISSDQAT 430
 DB 360 SVTKKIDDTIFQNPVGVGALMGFNFDIKYTMEEKIQ---TSGS-NYLSLEVLADLVS 415

RESULT 14

ID BIR4_HUMAN STANDARD; PRT: 497 AA.
 AC P98170; O9N014;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Baculoviral IAP repeat-containing protein 4 (inhibitor of apoptosis protein 3) (X-linked inhibitor of apoptosis protein) (X-linked IAP)
 DE (IAP-like protein) (HILP)
 GN BIR4 OR AP13 OR IAP1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=96149249; PubMed=8552191;
 RA Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertnon-Horvat G., Parahani R., Mclean M., Ikeda J., Mckenzie A., Korneluk R.G., "Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes.";
 RT Nature 379:349-353(1996).
 RL

RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal heart;
 RX MEDLINE=96256286; PubMed=8654366;
 RA Duckett C.S., Nava V.E., Gedrich R.W., Clem R.J., van Dongen J.L., Giffillan M.C., Shields H., Hardwick J.M., Thompson C.B.;
 RT "A conserved family of cellular genes related to the baculovirus IAP gene and encoding apoptosis inhibitors.";
 RL EMBO J. 15:2685-2694(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Graham D.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP FUNCTION
 RX MEDLINE=97373959; PubMed=9230442;
 RA Deveraux Q.L., Takahashi R., Salvesen G.S., Reed J.C.;
 RT "X-linked IAP is a direct inhibitor of cell-death proteases.";
 RL Nature 388:300-304(1997).
 CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. INHIBITOR OF CASPASE-3 AND CASPASE-7.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: UBICUITOUS, EXCEPT PERIPHERAL BLOOD LEUKOCYTES.
 CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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 CC
 DR EMBL; U45880; AAC50373.1; -;
 DR EMBL; U32974; AAC50518.1; -;
 DR EMBL; AL121601; CAB95312.1; -;
 DR HSSP; Q13490; 10BH.
 DR MIM; 300079; -;
 DR InterPro; IPR001370; BIR.
 DR InterPro; IPR001841; Znf_fing.
 DR Pfam; PF00653; BIR. 3.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00238; BIR. 3.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS01282; BIR_REPEAT_1; 3.
 DR PROSITE; PS0143; BIR_REPEAT_2; 3.
 DR PROSITE; PS00518; zf_RING_1; FALSE_NEG.
 DR PROSITE; PS00089; zf_RING_2; 1.
 KW Apoptosis; zinc-finger; Repeat; Thiol protease inhibitor.
 FT REPEAT 26 93 BIR 1.
 FT REPEAT 163 230 BIR 2.
 FT REPEAT 265 330 BIR 3.
 FT ZN_FING 450 485 RING-TYPE.
 FT CONFLICT 162 162 S->C (in Ref. 1).
 FT CONFLICT 423 423 Q->P (in Ref. 2).
 SO SEQUENCE 497 AA; 56684 MW; 9D394C16D45EB635 CRC64;

Query Match 5.6%; Score 407; DB 1; Length 497;
 Best Local Similarity 30.0%; Pred. No. 5.7e-17;
 Matches 124; Conservative 59; Mismatches 152; Indels 78; Gaps 19;

QY 60 EAKRLKFTVTEPYSSWIPQMAAGFYFTGKSGICFCSCSLIFGAGLTRLPED--- 116
 DB 26 EFNRLKFTFANPPSSPVASLTLARAGFLYTGEGDTRCFSCS-----AAVDRMVGDSAV 80
 QY 117 --HRRFHDGCF-----GNIAKYDIRKN-LKSR----- 148
 DB 81 GRHRVSPNCRFINGFYLENSATOSTSGIONGQYKVENYLGSRDHPALDRPSETHADYL 140

```

QY 149 LRGM-----RYOEEARLAFRNPFFVYOGISPCVLSAGVFTKODTQV 196
Db 141 LRTQVVDISDTIYPRNPAMYSEARLAKSFQNPDPYAH-LTPRELSAGIYYTGIDQVQ 199
QY 197 CFSCGGCGGNNWEGDDPWKEIAKWPFCFELRSKSSSEITTOYOSKGFVDITGHPV 256
Db 200 CFCCGGGLKNNWEPDRAMSEHRRFPNCFVLRNLN-----IRSEDAVS-SDNFPN 252
QY 257 SWOARELPMAAYCNDSTIFAYEELRLDSEKDFRESAVGVAALAKGLTYTGIDVOCF 316
Db 253 S---TNLPR-----NPSMADY-EARIFFTGTW--ITSVAKKQOLARAGFALGEGDKVCF 301
QY 317 SCGGGCEKQWEGDDPLDDHTRCFNCPFLQNNKSSAEVTPDLSQSGELCELLETTSSES-- 374
Db 302 HCGGGLTDMKPSDDPWQIAKWPFCCKYLLDQKGQ-EYINIHILHSLSECLVTRTEKTP 360
QY 375 -----NLEDSTAVGPVPE-MAQGEAOMFOEAKNLNDOLRAATSAFRRMSLL 422
Db 361 SLTRRIDDTIFQNPVQEAIRMGFS--FKDIKIME-KIQTSGSNYSLEVL 410

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RESULT 15

BIR_CHICK STANDARD: PRT: 611 AA.

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AC Q90660:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inhibitor of apoptosis protein (IAP) (inhibitor of T cell apoptosis
protein).
GN ITA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OX NCBI_TaxID=9031;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=9710112; PubMed=8945639;
RA Digby M.R., Kimpleton W.G., York J.J., Connick T.E., Lowenthal J.W.;
RT ITA, a vertebrate homologue of IAP that is expressed in T
RL DNA Cell Biol. 15:981-988(1996).
CC - FUNCTION: APOPTOTIC SUPPRESSOR (BY SIMILARITY).
CC - CELLULAR LOCATION: PREDOMINANTLY NUCLEAR.
CC - TISSUE SPECIFICITY: CELLS OF THE T LYMPHOCYTE LINEAGE. FOUND IN
CC BOTH CORTICAL AND MEDULLARY CELLS OF THE THYMUS.
CC - DEVELOPMENTAL STAGE: HIGH LEVELS ARE INDUCED WITHIN 4-8 HOURS OF
CC T-CELL ACTIVATION IN SPLEEN AND THYMUS.
CC - SIMILARITY: BELONGS TO THE IAP REPEATS.
CC - SIMILARITY: CONTAINS 3 BIR REPEATS.
CC - SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR HSSP; Q13490; 10BH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; ZnF_fing.
DR Pfam; PF00653; BIR; 3.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 3.
DR SMART; SM00114; CARD; 1.

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DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 3.
DR PROSITE; PS0143; BIR_REPEAT_2; 3.
DR PROSITE; PS0209; CARD; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Apoptosis; Zinc-finger; Repeat; Nuclear protein.
FT REPEAT 30 97 BIR 1.
FT REPEAT 176 242 BIR 2.
FT REPEAT 262 329 BIR 3.
FT DOMAIN 446 536 CARD.
FT ZN_FING 564 599 RING-TYPE.
SQ SEQUENCE 611 AA; 69009 MW; 53FC9136F34EBDD CAC64;

```

Query Match Best Local Similarity 5.3%; Score 388; DB 1; Length 611; Matches 142; Conservative 86; Mismatches 207; Indels 184; Gaps 21;

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QY 60 EAKRLTFVYEPYSSMIFQEMAAAGFYFTGKSGIOCFCCSLIFGAGLRLPIEDHR 119
Db 30 ELYRMSTFTFPVNPVNSRRRLARAGFYITGVQDKVCFSGGLYLDNMPGDNAMEKHQ 89
QY 120 FHPDGGFLN-----RDYGN----- 135
Db 90 VTPSCSFVQNMLSLNLGLSTHSAFSPVANSLSPLRSMTLSPSEFGVYGFSGSFSSFP 149
QY 136 -----AKYDIRVKNLSRLRGKMRQFEARLASRRNPFVVOGISPCVSEAGFVP 188
Db 150 RDPVTTAAEDL--SHLSKLNPSM--STEARLRYSNAP--LMCLMPAEVAKALD 203
QY 189 TGKOTVOCFSCGGCLGWMEBCDDPWKEIAKWPFCFELRSKSSSEITTOYOSKGFVD 248
Db 204 LGTAKVACVNCVGLKLSMBEPRDNAMSEHRRHFPNCFVEN----- 244
QY 249 ITGEHFVSNVQARELPMAAYCNDSTIFAYEELRLDSEKDFRESAVGVAALAKGLTYTG 308
Db 245 -----LMRDP--SFVSNVNTQTHARKKTFINPPTIPVQPEQLADAGFYVG 292
QY 309 IKDIVOCFSCGGCGGCKLEKQWEGDDPLDDHTRCFNCPFLQNNKSSAEVTPDLSQR-----G 362
Db 293 RNDVRCFCDCGGGLRCWESGDDPWIEIAKWPFCFELRSKSSSEITTOYOSKGFVD 351
QY 363 ELCELLETTSSENLDSIAVGPVPEMAQGEAOMFOEAKNLNDOLRAATSAF----- 416
Db 352 SSC-----TSDKPYDEN--MDPII-HPEGESP-SEDAIMNTPVVKAALMGFSRRLIK 403
QY 417 -----RMSLIDSSDLAT-----DHLLGCDLSIAKHSKIPVQ 450
Db 404 QTVOSKLTAEENYKTVNDVLSLTAEDKEKEKEQFEVVASDDLSLKN----- 457
QY 451 EPLVLEVEFGNLNVACVEGASGK-----TVLAKIAF 485
Db 458 -----RMALFORLTVSVPILGSLLSAKVITELHDVIAKOTTPQSOARELIDIVKGNAA 513
QY 486 LMASGCCPLNRFOLVFLYSLSSTR-----PDEGLASIIDOLEK--EGSVTECMKNI 538
Db 514 ASIFRNC--LKQFDPLVYKDLFVEKSMKYVPEDVSGLPMEQRLRLOBERTCKVCDKE 571
QY 539 IQQLKQVFLFLDDYKEIG 557
Db 572 V-----SIVFICGHLVYC 585

```

Search completed: September 30, 2002, 15:07:03
Job time: 184 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 30, 2002, 15:01:49 : Search time 31.33 Seconds
(without alignments)
4303.011 Million cell updates/sec

Title: US-09-830-338-1

Sequence: 1 MATOQKASDERISQFDHNL.....SKYLTILOKWLIFSPITIQK 1403

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: PIR-71:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6373.5	87.2	1232	2 A55478	neuronal apoptosis
2	4919	67.3	1447	2 T42628	neuronal apoptosis
3	462	6.3	618	2 S68450	apoptosis inhibito
4	431.5	5.9	604	2 S68449	apoptosis inhibito
5	407	5.6	497	2 S69544	apoptosis inhibito
6	345.5	4.7	497	2 S69545	apoptosis inhibito
7	332	4.5	496	2 S68452	apoptosis inhibito
8	326	4.5	358	2 JC5964	apoptosis inhibito
9	303.5	4.2	275	2 A45679	inhibitor-of-apopt
10	293.5	4.0	268	2 T10304	inhibitor of apopt
11	293.5	4.0	268	2 A53989	apoptosis-inhibiti
12	242.5	3.3	298	2 JC7568	kidney inhibitor o
13	241	3.3	1215	2 H84513	probable disease r
14	198	2.7	1192	2 T17255	hypothetical prote
15	194.5	2.7	997	2 T43523	cult1 protein - fi
16	192	2.6	1454	2 S48264	protein kinase VPS
17	181	2.5	1304	2 G85188	disease resistance
18	180.5	2.5	1041	2 C85189	disease resistance
19	178.5	2.4	1152	2 T31911	hypothetical prote
20	178.5	2.4	1317	2 B85189	disease resistance
21	177	2.4	1184	2 H71436	hypothetical prote
22	177	2.4	1294	2 T18546	flax rust resistanc
23	177	2.4	1301	2 D85188	apoptosis-inhibiti
24	175.5	2.4	275	2 T10310	conserved hypothet
25	175	2.4	1830	2 E82909	disease resistance
26	175	2.4	1895	2 T06609	disease resistance
27	175	2.4	2467	2 D71437	probable resistance
28	168.5	2.3	1257	2 T06269	root-knot nematode
29	168	2.3	292	2 T41772	IAPI orf27 - Bomby

30	167.5	2.3	1837	2 T41023	probable nuclear p
31	167	2.3	4540	2 T30838	cytoplasmic dynein
32	165.5	2.3	286	2 D36828	orf13 protein - Au
33	165.5	2.3	1253	2 T45787	disease resistance
34	164.5	2.2	1134	1 A29944	chaoptin precursor
35	162.5	2.2	1590	2 B86398	protein T7N9.24 [1
36	162.5	2.2	2335	2 T40186	probable phosphati
37	161	2.2	789	2 T52067	hypothetical prote
38	161	2.2	1110	2 F84547	probable disease r
39	160	2.2	150	2 T28409	ORF MSV248 probabl
40	160	2.2	919	2 T05746	hypothetical prote
41	159.5	2.2	624	2 T28423	ORF MSV261 leucine
42	159	2.2	1019	2 C96519	probable disease r
43	159	2.2	1802	2 T00020	bacterial blight-r
44	159	2.2	4639	1 A54794	dynein heavy chain
45	159	2.2	4717	2 T41581	hypothetical coile

ALIGNMENTS

RESULT 1

A55478 neuronal apoptosis inhibitory protein - human

N:Alternate names: NAIP

C:Species: Homo sapiens (man)

C>Date: 05-Jan-1996 #sequence, revision 05-Jan-1996 #text, change 02-Feb-2001

C:Accession: A55478

R:Roy, N.; Mahadevan, M.S.; McLean, M.; Shuttler, G.; Yareghli, Z.; Farahani, R.; Balid
d, T.O.; de Jong, P.J.; Surh, L.; Ikeda, J.E.; Korneluk, R.G.; Mackenzie, A.
Cell 80, 167-178, 1995

A:Title: The gene for neuronal apoptosis inhibitory protein is partially deleted in 1
A:Reference number: A55478; M01D:95112344

A:Accession: A55478

A:Molecule type: mRNA

A:Residues: 1-1232 <ROY>

A:Cross-references: GB:U19251

C:Genetics:

A:Gene: GDB:SMN6, SMA

A:Cross-references: GDB:120378; OMIM:600354; OMIM:253300

A:Map position: Sq12.2-Sq13

C:Keywords: apoptosis; ATP; glycoprotein; nucleotide binding; P-loop; transmembrane P

F:94-110/Domain: transmembrane #status predicted <TM1>

F:470-477/Region: nucleotide-binding motif A (P-loop)

F:479-486/Domain: transmembrane #status predicted <TM2>

F:476/Binding site: ATP (Lys) #status predicted

F:618,632,823,923,1035/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.2% Score 6373.5 DB 2: Length 1232:
Best Local Similarity 95.9% Pred. No. 0:
Matches 1229: Conservative 1: Mismatches 1: Indels 51: Gaps 1:

QY	1	MATQKASDERISQFDHNLPELSALGLDAVOLAKLEEBEORERAKMQGYNSQMSSE 60
DB	1	MATQKASDERISQFDHNLPELSALGLDAVOLAKLEEBEORERAKMQGYNSQMSSE 60
QY	61	AKRLKTFVTEYSYWIQEMAAAGFTYGKSGIQCCCSLLFGAGLTRLPIEDHRF 120
DB	61	AKRLKTFVTEYSYWIQEMAAAGFTYGKSGIQCCCSLLFGAGLTRLPIEDHRF 120
QY	121	HPDGFLLNKDVGNIAKVDIVKLNLSRLRGKMYOEERLASFRRMPPYVGISFCV 180
DB	121	HPDGFLLNKDVGNIAKVDIVKLNLSRLRGKMYOEERLASFRRMPPYVGISFCV 180
QY	181	LSEAGFVFTGRQDFTVQCSGCGCLGMEEGDPMKEHAKMPKCEFLRSKSSSEITQYI 240
DB	181	LSEAGFVFTGRQDFTVQCSGCGCLGMEEGDPMKEHAKMPKCEFLRSKSSSEITQYI 240
QY	241	QSYKGFVDITGEHFNYSVQRELPMASAYCNDISFAIYELRLDSFKDMPRESAVGVALA 300
DB	241	QSYKGFVDITGEHFNYSVQRELPMASAYCNDISFAIYELRLDSFKDMPRESAVGVALA 300

```

QY 301 KAGLFTGKIDIVQCFSCGCGLEKNOEGDDPLDHTRCFPNCPFLQNNKSSAEVTPDQS 360
DB 301 KAGLFTGKIDIVQCFSCGCGLEKNOEGDDPLDHTRCFPNCPFLQNNKSSAEVTPDQS 360
QY 361 REBELCELETTESNLESDIAVGPVIPMAQGEAOMFEAKNLNDEQLRAATSAFRHMS 420
DB 361 REBELCELETTESNLESDIAVGPVIPMAQGEAOMFEAKNLNDEQLRAATSAFRHMS 420
QY 421 LDISSDIATDHLGCGDLSIASKHSKRPQEPVLPEVFGNLSVMKVEGASGKTVLL 480
DB 421 LDISSDIATDHLGCGDLSIASKHSKRPQEPVLPEVFGNLSVMKVEGASGKTVLL 480
QY 481 KKIAPLMAAGCCPLNRPQVLEYLSSTRPDEGLASIIDOLIEKGVTEKMRNITQ 540
DB 481 KKIAPLMAAGCCPLNRPQVLEYLSSTRPDEGLASIIDOLIEKGVTEKMRNITQ 540
QY 541 QLKNOVLFLLDDYKEICSPQVIGKLIQKNHLSRTCLLIARTNRARDIRRYLETILEIQ 600
DB 541 QLKNOVLFLLDDYKEICSPQVIGKLIQKNHLSRTCLLIARTNRARDIRRYLETILEIQ 600
QY 601 AFPPYNTVCILRLKFSHNMTRLRKFWYFGKNOSLOKIQKTPLEVAICAHFQYPPDPS 660
DB 601 AFPPYNTVCILRLKFSHNMTRLRKFWYFGKNOSLOKIQKTPLEVAICAHFQYPPDPS 660
QY 661 FDDVAVFKSTWERYLSRNKATAEILKATVSSCGELAKGFSCCFEPNDLAEAGVDE 720
DB 661 FDDVAVFKSTWERYLSRNKATAEILKATVSSCGELAKGFSCCFEPNDLAEAGVDE 720
QY 721 EDLTWCLMSKFTQRLRPYRFLSPAFORFLAGMLIELSDSDROHODLGLYHLKQINS 780
DB 721 EDLTWCLMSKFTQRLRPYRFLSPAFORFLAGMLIELSDSDROHODLGLYHLKQINS 780
QY 781 PMHTVAVNNFLNYSVLSBSTAGPKIVSHLHLVDNKESELENTSENDYKAKHQPESLQ 840
DB 781 PMHTVAVNNFLNYSVLSBSTAGPKIVSHLHLVDNKESELENTSENDYKAKHQPESLQ 840
QY 841 MOLLRLQMOICPOAFESVMSSEHLYLAKTAYOSNTVAACSPFVLOFLQGRITLIGALNT 900
DB 841 MOLLRLQMOICPOAFESVMSSEHLYLAKTAYOSNTVAACSPFVLOFLQGRITLIGALNT 900
QY 901 OYFPHRPESLSLSTHPIRPNKNTSPRAHPSVLETCFDSOYPTIDODVAFSEPMNEM 960
DB 901 OYFPHRPESLSLSTHPIRPNKNTSPRAHPSVLETCFDSOYPTIDODVAFSEPMNEM 960
QY 961 ERNLAEKEDNKSYMDOQRASPDLSGTWKLSPKQKIPCLEVDVNDIDVYGOMLETL 1020
DB 961 ERNLAEKEDNKSYMDOQRASPDLSGTWKLSPKQKIPCLEVDVNDIDVYGOMLETL 1020
QY 1021 MTVSASQRIEHLNHSRGFIESIIPALDELKASVTKCSISKLELSAAQOELLTLPSLE 1080
DB 1021 MTVSASQRIEHLNHSRGFIESIIPALDELKASVTKCSISKLELSAAQOELLTLPSLE 1080
QY 1081 SLEVSQTIQSDODIPRLQKFLCKELSLVDLEGNINVSFVDEEPPNFMHEKLLIQISA 1140
DB 1081 SLEVSQTIQSDODIPRLQKFLCKELSLVDLEGNINVSFVDEEPPNFMHEKLLIQISA 1140
QY 1141 EYDPSKLYKLIONSPLNHLKCNFFSDGSLMTMLVCKLTETIKRSDSFQAVPPVA 1200
DB 1141 EYDPSKLYKLIONSPLNHLKCNFFSDGSLMTMLVCKLTETIKRSDSFQAVPPVA 1200
QY 1201 SLNPFISLKIILNLEGOQFPDEETSEKFAVILGSLNLEELLTPPGDGIYRAKLLIQOCC 1260
DB 1201 SLNPFISLKIILNLEGOQFPDEETSEKFAVILGSLNLEELLTPPGDGIYRAKLLIQOCC 1260
QY 1261 QLHCLRVLSFFFTLNDSDVET 1282
DB 1261 QLHCLRVLSFFFTLNDSDVET 1282
QY 1210 QLHCLRVLSFFFTLNDSDVET 1231
DB 1210 QLHCLRVLSFFFTLNDSDVET 1231

```

RESULT 2
 T42628
 neuronal apoptosis inhibitory protein 2 - mouse
 C:Species: Mus musculus (house mouse)

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
 C:Accession: T42628
 R:Ratghgh, Z.; Dlez, E.; Gros, P.; MacKenzie, A.
 Mamm. Genome 10, 761-763, 1999
 A:Title: CDNA cloning and the 5' genomic organization of Naip2, a candidate gene for m
 A:Reference number: 222179; MUID:99315342
 A:Accession: T42628
 A:Status: preliminary; translated from GB/EMBL/DDJ
 A:Molecule type: mRNA
 A:Residues: 1-1447 <TAR>
 A:Cross-references: EMBL:AF102871; NID:93860228; PID:93860229; PIDN:AAC73002.1
 C:Genetics:
 A:Gene: Naip2

```

Query Match          67.3%; Score 4919; DB 2; Length 1447;
Best Local Similarly 65.4%; Pred. No. 5e-301;
Matches 946; Conservative 180; Mismatches 277; Indels 44; Gaps 2;

QY 1 MATOQKASDERISQFQHNILPELALLGLDAVOLAKELEBEDOKERANKQKNSOMRSE 60
DB 1 MAOGEAVEEIIICEFDDLVSELSTLRYDALSVLRQDEEDHKTRMKKGFNSQMRSE 60
QY 61 AKRLKFTVYTERYSNIPQEMAAAGFYFYGKSGIQCFCCSLIFGAGTLPLIEDHKRF 120
DB 61 AKRLKFTFYDQFRSWTPQEMAAAGFYHTGVKLVQVCFCCSLIFSTLRKLPLEHKKL 120
QY 121 HPDCGFLNKRQDNIAKYDIRVKNLSRLRGKMKYQDEERARLASFRNRPYVGISPCV 180
DB 121 RECEPFLKQDVGNIGKIDIRKSPKEMLRKQKAYHEERARLESFDDMFYAHGTSFV 180
QY 181 LSEAGFVFGKDDYVQCCSCGCGCAGNMBEGDDPKKEHAKMFPKCEPLRSKRSBEITQY 240
DB 181 LSAAGFVFTGKRDYVQCCSCGCGCAGNMBEGDDPKKEHAKMFPKCEPLRSKRSBEITQY 240
QY 241 OSYKGFVDITGEHFVNSVQRELPMASAYCNDISFATLELRSLDSFKWPRESAVGAALA 300
DB 241 OSYEGFLVHTGEHFVNSVQRELPMASAYCNDISFATLELRSLDSFKWPRESAVGAALA 300
QY 301 KAGLFTGKIDIVQCFSCGCGLEKNOEGDDPLDHTRCFPNCPFLQNNKSSAEVTPDQS 360
DB 301 KAGLFTGKIDIVQCFSCGCGLEKNOEGDDPLDHTRCFPNCPFLQNNKSSAEVTPDQS 360
QY 361 RGELCELETTESNLESDIAV----- 382
DB 361 HCAPLEAMETTSSENHDDAAVAHSTVVDVSPSEAQLEBASLSVLCRDQHSFAQGRG 420
QY 383 -----GPIVPEMAQGEAOMFEAKNLNDEQLRAATSAFRHMSLSDIATDHLGCG 436
DB 421 CASSGYTLPSFTDLQGEBAQWLQEARSLSEQLRDITYTKATFRMINLPYVSSLAGTDHLGCG 480
QY 437 DLSIASKHSKRPQEPVLPEVFGNLSVMKVEGASGKTVLLKIAFLMAAGCCPLN 496
DB 481 DVSIIKHSIQPQSGSLTIPRYFNSLNSVMKVEGASGKTVLLKIAFLMAAGCCPLN 540
QY 497 RQVLYVLSLSTRPDEGLASTICDQLEKESVYEMKMRNITQOLKNOVLFLLDDYKEI 556
DB 541 RQVLYVLSLSTRPDEGLASTICDQLEKESVYEMKMRNITQOLKNOVLFLLDDYKEI 556
QY 557 CSTIPQVIGKLIQKNHLSRTCLLIARTNRARDIRRYLETILEIAFPYNTVCILRKF 600
DB 601 ASLPOLHLITLKKNVLSRTCLLIARTNRKNGIRPYLDTSLTEKEFPFYNTVSVLRKLP 660
QY 617 HNMTRLRKFWYFGKNOSLOKIQKTPLEVAICAHFQYFPDSDFDVAVFKSTWERYLS 676
DB 661 HDIMRVKRFINYPGFHELDQIHKTPLEVAACVDMKKNSDPFDVAVFKAYMAYLSL 720
QY 677 RNKATAEILKATVSSCGELAKGFSCCFEPNDLAEAGVDEDEDLTWCLMSKFTQRL 736
DB 721 KHKGAAPFLQATVSSCGELAKGFSSCFEPNSDNLAEAGVDEDELTWCLMSKFTQRL 780
QY 737 RPYRFLSPAFORFLAGMLIELSDSDROHODLGLYHLKQINS PMHTVAVNNFLNYSV 796

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Db 791 RPYVFLPLRQEFLLAVRLTELLSSDRQEDDGLLYLRQINSPLKAMSIYHTELYYS 840
Oy 797 SLSPKAGPKIVSHLLHYDNKRESLENTENDYLKHQPEISLOMQLRGIMQIQPQAVF 856
Db 841 SHPSKAPATVYSHLDLVDEKESLENSENEDYKMLHPEALLWTECRGMOLSPESPS 900
Oy 857 SMVSEHLLVLAKTAYQSNVTAACSPVLOFQGRITLTGALNLOYPDPHPSLSLNSI 916
Db 901 LPISENLRICINFHESNTVAACSPVILQFLRGRTLDLKVSLQYFNDHPHTLLLSI 960
Oy 917 HFPINGNTSPRAHVSLETSCDKSOVPTIDODVAAFEPMNEMERNLAEKEDNVKSYMD 976
Db 961 KISLNNMNVORIDSELSLEKSEPKVQPTIDODVAAICQPINEVOKNSEKHIIKKYED 1020
Oy 977 MORASPDLSITGYKWLKSKQYKIPCLEVDYNDIDVVGDMLEITLWVSASRIELHLNH 1036
Db 1021 MKHQPLNISTGYKWLSPKPKIPLEVOYNTGPAQDALLQVLMIEVVSASQIEFRISD 1080
Oy 1037 SRGFIESIRPALELSKASVTKCSISKLELSAEQELLTLPLSLEUSGTQSDQDIFP 1096
Db 1081 SSGFIESIRPALELSKASVTKCSMRLELSREDQKLLTLPLQSLSEVETQQLPDLFH 1140
Oy 1097 NLDFELCLKELESDLEGNINVSFVPEEPFNHMEKLLIOLISAEYDPSKVLKIQNSPN 1156
Db 1141 NLHKEFLGELKELCVRLDSKPDVSLPGEFPNLHMEKLSIRSTESDSLKLVKLIQNSPN 1200
Oy 1157 LHVFLKCNFSPDSGLMTMLVSCKKLTKRKSDSPFOQAVPVVALPNIISKLINLEBO 1216
Db 1201 LHVFLKCNFSPDSGLMTMLVASCCKLTKRKSDSPFOQAVPVVALPNIISKLINLEBO 1260
Oy 1217 QPPDETESEKFAVILGSLSNLEELLPTGQGIYRAKLIIOOQOOLHCLRVLSPEFTLND 1276
Db 1261 QPPDETESEKFAVILGSLSNLEELLPTGQGIYRAKLIIOOQOOLHCLRVLSPEFTLND 1320
Oy 1277 DSVETIAKVAISGGFQOKLEMLKLSINHKTKEGYRNFFQALDNMPNLOELDISRHEPTECI 1336
Db 1321 DSVETIAKVAISGGFQOKLEMLKLSINHKTKEGYRNFFQALDNMPNLOELDISRHEPTECI 1380
Oy 1337 KAOATVKSLSQCVLRPLRLRLNMLSMWLDADTALNVMERHPOSXYLLTLQKWILP 1396
Db 1381 QOQATLVKALGGCVSLPSLRLGMLSMWLDDEEDIKVINDVNERHPOSXYLLTLQKWILP 1440
Oy 1397 FSPVIOK 1403
Db 1441 FSPVIOK 1447

```

RESULT 3

```

S68450
Apoptosis inhibitor hiap-2 - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000
C:Accession: S68450
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani,
Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of
A:Reference number: A58182; MUID:96149249
A:Accession: S68450
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-618 <LIS>
A:Cross-references: EMBL:U45879; NID:g1184317; PIDN:ACG50372.1; PID:g1184318
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: RING finger homology
C:Keywords: apoptosis; zinc finger
F:567-611/Domain: RING finger homology <RNG>

```

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Query Match 6.3%; Score 462; DB 2; Length 618;
Best Local Similarity 24.7%; Pred. No. 3.9e-21;
Matches 159; Conservative 93; Mismatches 238; Indels 154; Gaps 24;

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Oy 38 LEEBQKERAKQKQVNSQMRSEAKRLKTFVYEPYSSWIP--QEMAAAGFTYGVKSG 94
Db 28 LSDMTNNSKQKQKQYDSC-----LYRMSYTFPPACVPYSEKSLARAGYYTGVDK 80
Oy 95 IOCPCCSLIFGAGLTRLPEDHKRFPDPCG--LNRKQVNIKAYDIRVN----- 144
Db 81 VACFCGGLMDLWKMLGDSPIQKHQOLYPCSPITQMLVSAISLSTSKTSPMNSFAHSLS 140
Oy 145 -----LKSRL-----RGKMR--QEBARLASFPNMPFYVG 175
Db 141 PTLHSSLSFGSSSLPPNPLNSRAVEDISSRTNYPYSTAMSTEARFLTYHMP--LTF 198
Oy 176 ISPCVLSFAGFYFTGKODTVOCFSCGCGLEKMGSDPDDHTRCFNCPPLQMKSSAEYT 235
Db 199 LSPSLARAGFYITGPDVACFACGGLSNPEPDAMSEIRRFNCPPL---ENSLF 255
Oy 236 ITQYIOSYKGFVDITGEHFVNSWORELPWASAYCNDISIFAEELRLDSFKMDPRESAVG 295
Db 256 TLFPSIS-----NLMTQ-----HAARMRTFMYHPSVPVQ 286
Oy 296 VAAIKKAGLFYTGIDIVOCFSCGCGLEKMGSDPDDHTRCFNCPPLQMKSSAEYT 355
Db 287 PQLASAGFYVGRNDVACFCGCGLEKMGSDPDDHTRCFNCPPLQMKSSAEYT 345
Oy 356 PQLASAGFYVGRNDVACFCGCGLEKMGSDPDDHTRCFNCPPLQMKSSAEYT 414
Db 346 DEIQGRYPLHQLSTSTQTEEN--ADPPIIHGPGHS--SDAYMMNTVYVSALEM 402
Oy 415 SF-----RMSLIDISSD-----ADHLLGCDLSIAS 442
Db 403 GNRDLVKQTVLSKITTGENTKVNDIVSALNADEREKEKEKQAEEMASDLSLR 462
Oy 443 KHISKVQDPLVPYFGL--NSVMCEGASGKTYL--LKKIAFIASG----- 490
Db 463 KNRMLFQDLCTVPLPLDLMLANVINKQEHDIKQKQIPQARLIDITVVKGAAN 522
Oy 491 ----CCPLNRFQVYLSLSTR----PDEGLASIIDQLER--EGSVTEMCMRNI 539
Db 523 IRRNC---LKEIDSTLYKMLFVDPKNNKIPTEDVSGLSLEBQLRRLQERTCKVCMDREV 579
Oy 540 QQLKQVLFLLDDYKEISIPVYIGKLIQKNHLSRTCLIAVRT 583
Db 580 -----SVVFIPCGHLVVC---QECAPSLRKCPICRGIINGIVRT 615

```

RESULT 4

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S68449
Apoptosis inhibitor hiap-1 - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jul-2000
C:Accession: S68449
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani,
Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of
A:Reference number: A58182; MUID:96149249
A:Accession: S68449
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-604 <LIS>
A:Cross-references: EMBL:U45878; NID:g1184315; PIDN:ACG50371.1; PID:g1184316
C:Function:
A:Description: apoptotic suppressor
C:Superfamily: RING finger homology
C:Keywords: apoptosis; zinc finger
F:553-597/Domain: RING finger homology <RNG>

```

```

Query Match 5.9%; Score 431.5; DB 2; Length 604;
Best Local Similarity 24.5%; Pred. No. 3.2e-19;
Matches 147; Conservative 83; Mismatches 201; Indels 169; Gaps 23;
Oy 69 TPEPYSSWIP--QEMAAAGFTYGVKSGIOCFCCSLIFGAGLTRLPEDHKRFPDPCG 125
Db 69 TPEPYSSWIP--QEMAAAGFTYGVKSGIOCFCCSLIFGAGLTRLPEDHKRFPDPCG 125

```

```

Db      35 TYSTFAGVPSVSESLARAGFYTGVDNDKVKFCGGLMDNWKRGDSPTKHNKLYPSCR 94
QY      126 FLIN-KDVONI-----AKYDIRKN-LKSLR-----150
Db      95 FVQSLASVNNLEATSQPTFPSSVTHSHSLPCTENSGYFRGVSNSPNSPVSRAHQEP 154
QY      151 GCKMR-----YQEEARLASFRMPPEYVOGISPCVLEAGFVFOTKOTVOCFCGCGCL 204
Db      155 SALMSSSPCCNNNNENNAALLFTOTWP--LTFELSPDLARAGFYTGVDNVCFAAGGKL 212
QY      205 GNMEGDDPMKEHAKWPKCEFLRSKSSSEITOTYSTKGFVDITGEHFVNSVQRELP 264
Db      213 SNMEKCNAMSEHLRHPPKCPTEIENQ--LQDTSRTVVS-----NLS 251
QY      265 MASAYCNDISFAVEBELRLDSFKDMPRESAVGAALAKAGLFTGTIKDIYQCGCGGCL 324
Db      252 MQT-----HAARFTFFEMPSVLYNDEOLASAGFYTGVDNVCFAAGGKL 301
QY      325 MWDGDDPLDHTRCFPCNPLONMKSSAEVTPDLSRGLCELLETTSSES-----374
Db      302 WESGDDPWQIAKMFPRCEYLIRIKGQFIQVQASTPHLEOLLSTSDSCDENAESI 361
QY      375 -----NLEDSIANG-PIVEMAQGFQNFQKAKNLEQRAAYTSASFRHMSLUDS 425
Db      362 INLEPGEHSEDAIMMNTFV--NAAVEMGFSRLVQVQRIKILANGENR-----413
QY      426 SDLATDHLIGDLSIASKHISKPVQEDVLPEVFGNLSVCEVGEAGSGKTYLAKIAF 485
Db      414 NOLVLD-LNAMDELREREERATE-----EKESNDLLIRK-----449
QY      466 LMASCCPLNRFQVLEFLSSTRPEGL-ASITCDQ-----LLRK- 526
Db      450 -----NRMALFQHLTCVPIILDLSLTAGIINQSHVDYIKOTQTSIGARELIDTI 499
QY      527 --EGSVTEMCMRNITQOLK--NOVLELDDYK-----EISGIPQVICKLQKHNLSRTC 576
Db      500 LVKGNIAATVFRNSLDQEAVALYELHLEVOODIKYIPTEDVSLP--VEQRLRLPEBRTC 557

RESULT 5
569544
Apoptosis Inhibitor IAP homolog - human
C:Species: Homo sapiens (man)
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000
C:Accession: S69544; #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000
R:Duickett, C.S.; Nave, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gillilan, M.C.
A:Title: A conserved family of cellular genes related to the baculovirus iap gene and
A:Reference number: S69544; MUID:96256286
A:Accession: S69544
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-497 <DUC>
A:CROSS-references: EMBL:U32974; NID:91016687; PIDN:ANC50518.1; PID:91016688
R:LiJation, P.; Roy, N.; Tamai, K.; Lefevre, C.; Baird, S.; Cherton-Horvat, G.; Farhanli,
A:Title: Suppression of apoptosis in mammalian cells by NIP and a related family of IAP
A:Reference number: A59182; MUID:96149249
A:Accession: S68451
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-161, 'C', 163-422, 'Q', 424-497 <LIS>
C:Genetics:
A:Gene: IIP
C:Function:
A:Description: apoptotic suppressor.
C:Superfamily: Apoptosis Inhibitor IAP homolog; RING finger homology
C:Keywords: apoptosis; zinc finger
F:446-490/Domain: RING finger homology <RRN>

```

Query Match 5.6%; Score 407; DB 2; Length 457;

Best Local Similarity 30.0%; Pred. No. 8.2e-18;

Matches 124; Conservative 59; Mismatches 152; Indels 78; Gaps 19;

```

QY      60 EAKRLKTFVYERYSWIMPOEAAAGFYTGKSGIQCCSLILFAGLRLPIED---116
Db      26 EFNRLKTFANFPGSPVSASTLARAGFLYTGCQVRCFSCH-----AAVDRMOYDSAV 80
QY      117 --HKRHPDC-----GFLANKDY-----GNIKYDIRKN-LKSR-----148
Db      81 GHRKVSFWCRITNCFYLENSATQSTNGIQNGYKVENTLGRDHPALDRSETHADYL 140
QY      149 LRGCKM-----RYQEEARLASFRMPPEYVOGISPCVLEAGFVFOTKOTVOCFCGCGCL 196
Db      141 LMTGQVVDISDTYPRNPAMTSEARLKSQNPMDIAH-LTPRELASAGLYTGIGDQV 199
QY      197 CFSCGCGKLNMEGDDPMKEHAKWPKCEFLRSKSSSEITOTYSTKGFVDITGEHFVN 256
Db      200 CFCCGCKLNMEGDDPMKEHAKWPKCEFLRSKSSSEITOTYSTKGFVDITGEHFVN 256
QY      257 SWQRELPMSANCNDISFAVEBELRLDSFKDMPRESAVGAALAKAGLFTGTIKDIYQCF 316
Db      253 S-----TNLPR-----NPSMADY--EARIFFGTW--IYVAKEDOLARAGFYTGIGDQV 301
QY      317 SCGCGCLEKMOEGDDPLDHTRCFPCNPLONMKSSAEVTPDLSRGLCELLETTSSES--374
Db      302 HCGGGLTDMKPSDEDPWEHAKWPKCEFLRSKSSSEITOTYSTKGFVDITGEHFVN 360
QY      375 ---NLEDSIANGVPIPE-MAQGFQNFQKAKNLEQRAAYTSASFRHMSL 422
Db      361 SLTRRIDDTIFQNPVQEAIRMGFS--FKDIKIMEE-KIQISQSNKSL 410

RESULT 6
569545
Apoptosis Inhibitor IAP homolog - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69545
R:Duickett, C.S.; Nave, V.E.; Gedrich, R.W.; Clem, R.J.; van Dongen, J.L.; Gillilan,
A:Title: A conserved family of cellular genes related to the baculovirus iap gene and
A:Reference number: S69544; MUID:96256286
A:Accession: S69545
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-497 <DUC>
A:CROSS-references: EMBL:U32373; NID:91019116; PIDN:ANC47155.1; PID:91019117
C:Genetics:
A:Gene: IIP
C:Function:
A:Description: apoptotic inhibitor IAP homolog; RING finger homology
F:446-490/Domain: RING finger homology <RRN>

```

Query Match 4.7%; Score 345.5; DB 2; Length 497;

Best Local Similarity 26.2%; Pred. No. 6.1e-14;

Matches 114; Conservative 65; Mismatches 161; Indels 95; Gaps 16;

```

QY      57 MRSEAKRIKTFVYERYSWIMPOEAAAGFYTGKSGIQCCSLIL-----FGAG 108
Db      6 MELSARLATTFGEPLNAVASABDVLANGFPATGNLMECHFCVDRIDRWDYGDQVANG 65
QY      109 LTRLPIEDHKRFHPDCCFLNKNQ-VGNIKAYDIRKNLSRLRGKMKRYQEEA-----161
Db      66 -----HRRSPISCSWVLAIRHICGNV-----RSQESDNEGNSVYDSFESCSDDL 111
QY      162 ----RLASFRMPPEYVOGISPCVLEAGFVFOTKOTVOCFCGCGCLAKNMEGDDPMKEH 217
Db      112 LEANRLVTFKDW--NPNTTPOALAKAGFYTLNDRHAKCYWCKGVAKEKNDNAFEEL 169
QY      218 AKWPKC-----EFLRSKSSSEITOTYSTKGFVDITGEHFVNSVQRELPMA 268
Db      170 KRFPQCPVQNGPLIERATGKNLDE-----LGIQPTT-----LPLRK 208

```



```

Db      65  KMAPQCPFNK-----IDVCGSVITNNIQ-----NTTHTHTIGCA 101
Oy      275  ---FAVEELRLDSFKDMPRESAVGAALAKAGLFTYTGIDIVQCCSGGCLGMEEGDDP 331
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      102  HKPAAHGAARVKSFFHMPKRCMPROMADAGFFYTGVDNTRKCFYCDGGLKDMPEIDVP 161
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      332  LDDHTCFPNCPLFNQKMSAEVTPDLQSGELCELL-ETTSSENLDSIAVGYTPPE 368
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      162  MEQHVHMFPRCAVQVLKGRDYOYKVT---EACVLPGEINTVST---AAPVSEPIPE 213
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
TI0304
Inhibitor of apoptosis protein 3 - Orygia pseudotsugata nuclear polyhedrosis virus
C:Species: Orygia pseudotsugata nuclear polyhedrosis virus, OpMPV
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2000
C:Accession: TI0304
R:Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohmann, G.F.
Virology 229, 381-399, 1997
A:Title: The sequence of the Orygia pseudotsugata multineucleocapsid nuclear polyhedrosis
A:Reference number: 217011; MUID:97271300
A:Accession: TI0304
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-268 <AHR>
A:Cross-references: EMBL:U75930; NID:92934903; PIDN:AAG59034.1; PID:g1911281
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology
F:217-261/Domain: RING finger homology <RRN>

Query Match      4.0%; Score 293.5; DB 2; Length 268;
Best Local Similarity 30.5%; Pred. No. 4.5e-11;
Matches 68; Conservative 34; Mismatches 88; Indels 33; Gaps 6;

Oy      157  QEEELRLASFRNMPFYVQGISPCVLSAGVFTGKODTVQCFSGGCLGMEEGDDP 216
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      16  KKKARLGTYYNMP--VQFLEPSRMAASGFYLGRCDEVCAKCAKCYEITWVGDDP 73
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      217  HAKWPKCEFLRSKSSSEITQYIQSYKGFVDITGEHFVNSWQRELPMASAYCNDSTFA 276
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      74  HKRMAPCCPVRNNAHDT-----PH-----DRAPPARSAAHPO-YA 109
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      277  YEELRLDSFKDMPRESAVGAALAKAGLFTYTGIDIVQCFSGGCLGMEEGDDP 336
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      110  TEARLRTFAEMPRGLKORPEELAEAGFFYTGCGDKTRCCDGLKDMPEPDAPWQHA 169
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      337  RCFPNCPLFNQKMSAEVTPDLQSR--GELCELETTSSNLE 377
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      170  RWDRCREYVLLVGR-----DFVQRVMTACVVRADNNEPHIE 207
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
A53989
Apoptosis-inhibiting protein - Orygia pseudotsugata multicapsid nuclear polyhedrosis virus
C:Species: Orygia pseudotsugata multicapsid nuclear polyhedrosis virus, OpMPV
C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 15-Sep-2000
C:Accession: A53989
R:Blinbaum, M.J.; Clem, R.J.; Miller, L.K.
Virology 188, 2521-2528, 1994
A:Title: An apoptosis-inhibiting gene from a nuclear polyhedrosis virus encoding a polyP
A:Reference number: A53989; MUID:94187094
A:Accession: A53989
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-268 <BIR>
A:Cross-references: GB:L22564; NID:9456111; PIDN:AAB02610.1; PID:9456114
A:Note: Authors translated the codon TGG for residue 28 as Tyr, GAC for residue 50 as As
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology
F:217-261/Domain: RING finger homology <RRN>

Query Match      4.0%; Score 293.5; DB 2; Length 268;
Best Local Similarity 30.5%; Pred. No. 4.5e-11;

```

```

Matches 68; Conservative 34; Mismatches 88; Indels 33; Gaps 6;

Oy      157  QEEELRLASFRNMPFYVQGISPCVLSAGVFTGKODTVQCFSGGCLGMEEGDDP 216
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      16  KKKARLGTYYNMP--VQFLEPSRMAASGFYLGRCDEVCAKCAKCYEITWVGDDP 73
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      217  HAKWPKCEFLRSKSSSEITQYIQSYKGFVDITGEHFVNSWQRELPMASAYCNDSTFA 276
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      74  HKRMAPCCPVRNNAHDT-----PH-----DRAPPARSAAHPO-YA 109
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      277  YEELRLDSFKDMPRESAVGAALAKAGLFTYTGIDIVQCFSGGCLGMEEGDDP 336
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      110  TEARLRTFAEMPRGLKORPEELAEAGFFYTGCGDKTRCCDGLKDMPEPDAPWQHA 169
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      337  RCFPNCPLFNQKMSAEVTPDLQSR--GELCELETTSSNLE 377
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      170  RWDRCREYVLLVGR-----DFVQRVMTACVVRADNNEPHIE 207
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
JC7568
Kidney inhibitor of apoptosis protein - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: JC7568
R:Lin, J.H.; Deng, G.; Huang, Q.; Morser, J.
Biochem. Biophys. Res. Commun. 279, 820-831, 2000
A:Title: KiAP, a novel member of the inhibitor of apoptosis protein family.
A:Reference number: JC7568; MUID: 21092523
A:Contents: Fetal kidney
A:Accession: JC7568
A:Molecule type: mRNA
A:Residues: 1-298 <LIN>
A:Comment: This protein, a new member of the inhibitor of apoptosis protein family, p
C:Genetics:
A:Gene: KiAP
A:Map position: 20q13.3
C:Keywords: apoptosis

Query Match      3.3%; Score 242.5; DB 2; Length 298;
Best Local Similarity 43.5%; Pred. No. 8.5e-08;
Matches 54; Conservative 15; Mismatches 44; Indels 11; Gaps 4;

Oy      159  EEARLASFRNMPFYVQGISPCVLSAGVFTGKODTVQCFSGGCLGMEEGDDP 218
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      87  EELRLASFPPLTAE--VPEELAAAGFFHGHQDKVRCFCYGGIQSWKRGDDP 145
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      219  KWPCKCEFLRSKSSSEITQYIQSYKGFVDITGEHFVNSWQRELPMASAYCNDSTFA 276
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      146  KWPSCQFLRSKGRD-----FVHS-----VQETHSQLGSDMPHEBBDAPVAPSPASG 197
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      277  YEEL 280
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      198  YPEL 201
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
H84513
Probable disease resistance protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: H84513
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
et al.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Umayam, L.; Tallon,
et al.; Neff, M.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
et al. Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: H84513
A:Status: Preliminary
A:Molecule type: DNA

```

A:Residues: 1-1215 <STO>
 A:Cross-References: GB:AE002093; MID:96598711; PIDN:AAD25848.2; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g14080
 A:Map position: 2

Query Match 3.3%: Score 241; DB 2; Length 1215;
 Best Local Similarity 19.8%; Pred. No. 8,9e-07;
 Matches 226; Conservative 165; Mismatches 383; Indels 370; Gaps 52;

```

QY 368 LETTSSENLSDSIATVGPVPEMAAG-----EAGW----- 396
DB 84 IDFTIDNNIERSKISIGELIARIGSKIAVLLSKDYASSWMCNLEVEIKKGRMLDQT 143
QY 397 ----FOE-----AKNLEOURLAAYTSASFRHMSLIDSSLDADHLICDLS 439
DB 144 VMTIFVEYDPTDYKQGTGDFGVKVKTCMKTNVSRKMIALSEVATIAGEHSIMDTE 203
QY 440 IA-----SKHSKPVGEPLVPEVFG-----NLNSVVCVE-----GEAGSG 475
DB 204 AAMIEKSTSDISKNLNNSTPLRDPDGLVGMCAHMEKLELLCLDSCEYRMIGWPGPIG 263
QY 476 KTVLLKRIAFIMASGCCPLNRFOLVFL-----SLSTRPEGLASIIDOLEK-- 526
DB 264 KTTIVR--FLYNQ-----LSSSFELSTFMENIKMTHTLASDDYSAKLIIQRFPLSKIL 316
QY 527 EGSVTECMCRNIIOQ--LKNQVFLLDYKEICISIPQVIGLIIQKNLSRTCLLIIVFTN 584
DB 317 DHKDEIPIHLVLOERLYNKKVLVYLD-----VDOSVOLDALAKETRWFGPRS- 365
QY 585 RADIRRLRLEILKAFPPFNTVCILKLFSSHMTLRKPMYV-FEGNOSLOIKOTRP- 642
DB 366 -----KILITTOQRKLLKAHRINNIIKYVDLPNSDDAQLQICMTAFG-----OKTPY 411
QY 643 --LFEVAICAHMF--QYPPDFSPDVAVFKSYMERLSLRNKATAEI--LKATVSSCGELA 696
DB 412 DGFYKLRKRVTLVGNFPL-----GLRVGSYFREM--KQEMREIPLRLARLOKIESV 465
QY 697 LKGFSCCFEENDDLAEGVDEDEDLTMCMSKFTAORLRPFYRFLSPAQEFLAGRL 756
DB 466 LK-----FSYDALC--DEKDLFLHIACFNHESIKLEDFLKTPE----- 504
QY 757 IELDSROEHQDGLYHLKOINSRPMVTSAVNNPLNVSSLSPTKAGPKIV----- 808
DB 505 ---LDIAORFH-----VLAEKSLISINSFVEMHDSL--AQJKEIYRKQSVAP 549
QY 809 SHLLHVDNKESELENISENDYLRKQPEISLOMOLLRG--LMQICPOAYFSAVSEHLVL 866
DB 550 GQRFQVLDARDISEVLA--DDTAGGRSVYIGIYLDLHRNDVFNISEKAFEGM--SNLOFL 605
QY 867 ALKRAYOSNTVAACSPVYLOFLOGRTLTGLALNLOFYFDHSESLSLRSHFPIRGKNTS 926
DB 606 RVKRFNGLFPAIVCIPLCLYIS-----RKRLRLDMWMTFPM----- 641
QY 927 PRAHFSVLETCFDSQVPTIDQYASAEF-----MNEMERNLAEKEDNVASYMDMORA 981
DB 642 -----TGF-----PSKFNPEFLVELNMMGSKLEKMEIOPLRKLR-- 678
QY 982 SPDLSTGYWKLSPROYKIPCLEVDVNDIDVYGOMLEILMTVFSASQRIELHLNHSRGI 1041
DB 679 -----MDLFSKNLKELEPLDLSATNTLEVNLNMGCSLV 711
QY 1042 ESIRPALELSASTKCSIKLELSAEOELLLPLPSLESEVGTIOSOQOIPPNLDF 1101
DB 712 E-----LPFSIGNATK--LTKLELSGCS--LLELP--SIGNATVMIQTIIDSHCNL 758
QY 1102 L-----CLKEIADVLEGINVFSVPEEPFNFMHEKL-LIQISAETDSKVLKL 1150
DB 759 VELSSSIGNATNKLKELDLSGCSL--KELPSSIGNCTNKLKHLICSS--LKELPSS 812
QY 1151 IONSPLNHLVFLKC-----NFFSPGSLMTM--LVSCKRLTEIKFSDFEQAVPVAS 1201

```

```

DB 813 IGNCTNLKELHLTCCSSSLIKLPSSIGNALINLEKLIACESLVE----- 856
QY 1202 LPNFL-----SUKTIINLEEQQPPDETSERFAYILGSLNLEEL-----ILPTGGCI 1248
DB 857 LPSPFGKATNKTILNGLVLSCLVLEPS-----FTGNLKRISLELRGCKRQVLPNTNL 911
QY 1249 YRVAKLLIIQCCQILHCLVLSFFFTLNDVSVEIAKVAISG-----GFOKLENTL 1297
DB 912 EFLNELDITDCLILKTPFVIS-----TNIKRHLRRTQILEVPSLSRSPRLLEDL 961
QY 1298 KLSINHKITEEGYRNFQALDNMPLOELDISRHFTECIKAKAATTVASLSOCVLRPLI 1357
DB 962 QMLXSENLS-----FSVILRITVLELSDIN-----IREMTPLMRITFLR 1003
QY 1358 RLNM 1361
DB 1004 RLKL 1007

```

RESULT 14

T17255
 hypothetical protein DKFZp58601822.1 - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T17255
 R:Koehler, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 Submitted to the Protein Sequence Database, September 1999
 A:Reference number: Z18722
 A:Accession: T17255
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1192 <KOE>
 A:Cross-References: EMBL:AL117470
 A:Experimental source: adult uterus; clone DKFZp58601822
 C:Genetics:
 A:Note: DKFZp58601822.1

Query Match 2.7%: Score 198; DB 2; Length 1192;

Best Local Similarity 20.8%; Pred. No. 0.00044;

Matches 158; Conservative 108; Mismatches 282; Indels 212; Gaps 34;

```

QY 450 QEPVL-----LPEVFG-NLNS-----VMCEGEGASGKTVLLKRIAFIM 487
DB 11 QDPLVKRSPDYVEENRGLHLEIRDFPGDLPQEPRIYIIQGAAGIKSTLQAQVKEAM 70
QY 488 ASGCCPLNRFOLVFLYLSLSTRPEGLASIIDOLEKEGSVTCEMCRNIIQOLKNQVL 547
DB 71 GRGQL-YGDRFOHVFYFSCRELAQSK--VYSLAEILIGDGTATPAPRIQLTSR-PERLL 125
QY 548 FLDDY-----KEIC--SIPO-----VIGKLIQKNLSRTCLLIIVRTRNADI 589
DB 126 FILDGVDEPGWVLOEPSELCLHNSQOPADALLGSLGKTIPEASFLIARTTALONTL 185
QY 590 RRYLETI--LEIKAFPPFNTVCILKLFSSHMTLRKPMYVFGKNOSLOKOTPLFVAA 647
DB 186 IPSLEQANWEVYLGFSSESREKRYPRYFTDERQAIRARL-VKSKELMALCLVPWWSHL 244
QY 648 ICAMHFOYPPDFSPDVAVFKSYMERLSLRNKAT-----AEIKATVSSCGE 694
DB 245 ACTCLMQQ-----MKRREKLTUTSKTTTTLCLHVAQALAQNPGLQRLDCLS 292
QY 695 LALKGFSCCFEENDDLAEGVDEDEDLTMCMSKFTAORLRPFYRFLSPAQEFLAGM 754
DB 293 LAAGELWOKTILFSPDDRKRGHLDAAIISTFLKGILOEHPIPLSYFIHLCFQEFFYAM 352
QY 755 RLIELDSDROEHQDGLYHLKOINSRPMVTSAVNNPLNVSSLSPTKAGPKIVSHLLHL 814
DB 353 SYVLEDEKGRKHSNC-IIDLEK-----TLEATG-----IHGL-----FGASTRFLFLGL 396
QY 815 V--DNKESLENI-----SENDYLRKQPEISLOMQ-----LLRGIMQICPOAYFSMSEH 862
DB 397 LSDEGEREMENIFHCRLSQGRNLQMWPISQILLQPHSLSLHCLYETRRNKTFLQVMAH 456

```

QY 863 L--LVALKTAYQSNVTAACSPF-----VLQFQGRITLGLALNQYFEDHPESSLSLRS 915
 Db 457 FEEMGMCEVETMELLVCTFCIKFSRNHKKLQLTIEGR-----QHSSTWSPIMV 503
 QY 916 IHPFRGNKTSIPRAHFSVLETCFCDKSCQVPTIDQYASAFEPNMEERNLAE-----K 967
 Db 504 VLF-----RMVPTDAVYMQILFSVL-KYTRNLKLEDDJSGNSLS 540
 QY 968 EDNYSKYMQRRA-----SPRLSTGYMKLSKQYKIPCLEVDYNDI 1009
 Db 541 HSAVSKSLKTLRRPCLLETLRLAGGLTAECQDLAFG---LRANQ-TTLELDLSFNVL 596
 QY 1010 DVG-----ODMEILMTFVSASQRI-ELHLNLS----- 1037
 Db 597 TDGAKHLICORLQPSCKIQRLQVSCGLTSPCCODLASVLSASPSLKELDLQONNDVY 656
 QY 1038 --RGFTESIR-PALELSKASVTKCSIS---KLELSAEOE 1071
 Db 657 GYRLCEGLRHAPACKLIRLIGDQTTLSDEMQRLEALOE 636

RESULT 15

T43523

cut17 protein - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 02-Jun-2000
 C:Accession: T43523; T41649; T41700
 R:Motilula, J.; Matsusaka, T.; Yanagida, M.
 submitted to the EMBL data library, August 1999
 A:Description: Fission yeast cut17 is required for chromosome segregation.
 A:Reference number: 222536
 A:Accession: T43523
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-997 <MOR>
 A:Cross-references: EMBL:AB031034; PIDN:BA8415.1
 R:Barrell, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL data library, August 1998
 A:Reference number: 222007
 A:Accession: T41649
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-997 <HAR>
 A:Cross-references: EMBL:AL031323; PIDN:CAA20434.1; GSPDB:GN00068; SPDB:SPCC962.02c
 R:Medler, H.; Duesteroheft, A.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL data library, October 1999
 A:Reference number: 222010
 A:Accession: T41700
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 932-997 <MED>
 A:Cross-references: EMBL:AL121859; PIDN:CA58376.1; GSPDB:GN00068; SPDB:SPCP11B10.10c
 C:Gene(s):
 A:Gene: cut17; SPCC962.02c; SPDB:SPCP11B10.10c
 A:Map position: 3L
 A:Introns: 43/3

Query Match

Best Local Similarity 2.7%; score 194.5; DB: 2; Length 997;
 Matches 232; Conservative 177; Mismatches 447; Indels 365; Gaps 60;

QY 147 SRLRGKMYQEEEARLSF--RAMPFYVQGISPCVLSGAGFVTT-----GKDDTVQ 196
 Db 13 NRRFRMCMYK---RLDTFOKKWPRAP--TPETLATVGFYINPISSEENSEERLDNVT 67
 QY 197 CSCGGCCGNNMEEDDPKPKHAKWPKCEPLRSKSSSELTQYQYKGFVDITGHEFVN 256
 Db 68 CYMCKSFYDWDDEDDPLKEHITHSPSCPW-----AVILSSK-----N 105
 QY 257 SWVGRELPMASAYCNDISFATVEELRLDSFRDMPRESAVGVALAKAGLGY---TGKIDLIV 313

Db 106 NPNQNOAALTKRCRCQTFVQKWPYTNRPDYHCEPSV---MAASGFVNPAPKADKA 161
 QY 314 OCFSGCCGCKLEKQOEEDDPLDHTTRCFPCFPLOMMKSSAEVTPLOSRGLCELETTSE 373
 Db 162 RCLYCDINLHMEPEDDPDYTEKRRACVFF-TWKPNSLSIPKLS-----ELSTSN 213
 QY 374 SNLEDSIANGPIVPEMAQGEAOWFOEAKNLEOLRAAYTSASFRHMSLDDISSDLATDHL 433
 Db 214 IDPEDLTEDNSILPSPTRDST--KSHKTLN-----FSPSRKNNNANRPLMSLT 262
 QY 434 LGCDLSIAKSIIRPVQ-----EPVLV-----PEVGNLNSWCJEGEAG 473
 Db 263 ---NTSEEDSOPTRAPQSPTRPVLLTPRRKKNKSPKSKPAPYKVPKPTFSDDEDD 317
 QY 474 SGKTVLLKRIAFVLAASGCC-----PL-----NRQLVFYLSLSTRPDE 513
 Db 318 DDLTA-----SOPFSKICNDMSQVAKKNFTETPLKEDEKDNLE---HLVSPATSVHT 369
 QY 514 GLASIIICDOLLEKEGSTECM---RNIIQQLKNOVLFLDDYKEICSIPOVIGKILQK 569
 Db 370 TVSDITGHQSVTVDESEONNCMSTPKIEIESKIEBISVYSKSEISSVSVGK--EQ 427
 QY 570 NULSRICLLIAYTNRRARDIRRYLEIKAFFRYNTVCLRLKLFSHNMTRLRKMYVF 629
 Db 428 NHTKQ---VAIETTPROKVERKEDEHL-----NLOGSFTEESTK----- 463
 QY 630 GKNQSIQKIQKTPLEVAICAMHFOYPPDPSPDDVAV---FKSYMERLSLNKKAET 684
 Db 464 -----QPISSRP-----STSSPDMTAAAGRVSSSPFDKILQTNFSP--- 502
 QY 685 LKATVSCGEALKGFSCFREFNDDDLAEGVDEDEDLMCMCSFTAORLRPPTRLUS 744
 Db 503 -NSTIDFSNISKRNSE---EANDR-----NDENLNTPIPEK-----K 538
 QY 745 PAFQFELAMRLIELELSDRQEHODLCLYLKQINSPIPMVSAVNNFLNYVSSLPSTAG 804
 Db 539 RKFOEVLQSKNI--LVSTEDSHEPV---KVTEDSOTAIHVSKEFLEN----- 582
 QY 805 PKIYSHLHLVDNKESELENI--SENDYLRHPEISLOQLRGLMOICPOAVFSWSEH 862
 Db 583 -----KSMESQSIQLLSESEND---KPLDL----- 607
 QY 863 LVLVLTAKTAVQSNVTAACSPFYVQLQGRITLGLALNQYFEDHPESSLSLRSHPFRIG 922
 Db 608 IPLAIKIR--KDLVSG---VLE--KCKSTSTSKTK--FD---TSYDFTL----- 646
 QY 923 NKTSPRAHFSVL-----ETCFDKSQVPTID-----QYASAF-----EPNEMERN 963
 Db 647 ---KPRTEISEVLPEEKRAICDESGYTRVSDKVTTRDVSPPVDEKSENNMEAN 703
 QY 964 LAEKEDNVKSYDMQRRASR-DLSTG-YWKLSP-----KQYKIPCLEVDYNDIDVYGQD 1016
 Db 704 SGHTVANNVHSSLDPPPIYOPELSEGSYLKDLPRRNGNSBKVYFOGDDINSKLOSKNN 763
 QY 1017 LELMTVFSASQRI-ELHLNHSRGFIESIRPALELSKASVTKCSIKLELSAA--EQELL 1073
 Db 764 QTVBAVNTETSDKLOEKEANHELENIKEKL-----TEVQVLSLSAFAFPQDEIK 814
 QY 1074 LTPLSLELVSGTIOGSDQDFFRLDKFLCLAKELSYDLEGNINVFSEVIREPNNHNEK 1133
 Db 815 NSRITSV---NGT-RVSKNTPF-----KETVYKDKIDNYSKKDY--ETSPGSCETSS 860
 QY 1134 LLIDISAYDPSKIVLQNSP-----NLHVFHLKCNFFDFGLMMLVLYSC 1180
 Db 861 AFAKTYAEKEVTST-----NLPSVRKPLDESYVDHSISFDPLCO--SSFLAPQTPYKSK 913
 QY 1181 KILTEIFSDSPFOAVPFAVL-----PNFISLKLMLGEOQFP-----D 1220
 Db 914 HALPVEANAPWEPRIIDFSLSLSEVPVNPVEPNKLSKELDMTEQVNIKPMYAKCAKEFE 973
 QY 1221 EHTSEKFAVILGSLNLEELI 1241

Tue Oct 1 09:27:21 2002

us-09-830-338-1.rpx

Page 9

Db 974 EACEKIEWLLEGGKRAEEYI 994

Search completed: September 30, 2002, 15:05:37
Job time: 228 sec

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Db      2 KKKKGNQSRSEAKRLKTEFTYDPRFMSWPOEMAAGFYHTGRLGVOCFCCSLTLFGN 61
Oy      108 GLTRLPIEDHKKRPHDCCGFLNKKDVGNIATKADIVKVLKSLRGKRRYOEDEARLASFR 167
Db      62 SLKKLPIERHKKLRPECELOGKDGKIDIRVKKRPMKMLKAGARHEEAEARLEFE 121
Oy      168 NMFYVQGISPCVLSAGFVFTGKQDVPVOCFSCGCLGNMGGDDPMKEHAKMPKCEFL 227
Db      122 DMPEFAHGTSPRYLSAAGFVFTGKRDYVOCFSCGCLGNMGGDDPMKEHAKMPKCEFL 181
Oy      228 RKSKSEETIYQISYKGFVDINGEFVMSWORELPMAVANDSIIPAYBELRLDSFKD 287
Db      132 QSKKSEETIYQISYKGFVDINGEFVMSWORELPMAVANDSIIPAYBELRLDSFKD 287
Oy      288 WPRASAGVAALAKGLFTGTGKIDYVOCFSCGCLGNMGGDDPMKEHAKMPKCEFL 241
Db      242 WPOESPVGEALVRAGFVFTGKRDYVOCFSCGCLGNMGGDDPMKEHAKMPKCEFL 301
Oy      348 MKSASVTPDLOSRLCELETTSESNELEDSITAVGPIYEMAGQRAQWFOAKNLNQL 407
Db      302 LKSSAVITPTLOSAYALPEATEETRESNHGDAAV----- 336
Oy      408 RAAYTSASRHHSLDISDLATDHLGCDLSIAKSHISKPVQEPVLVPEVFGNLNSVMC 467
Db      337 ----- 336
Oy      468 VEGAGSGKTVLKKIAFLWASGCCPLRLRFQVLFYLSLSTRDEGLASTICDQLLEKE 527
Db      337 ----- 336
Oy      528 GSVTMCMRNIIQOLKNQVLLDDYKEICSIPOVIGLLOKNNLSRTCLLAIVRTNRAR 587
Db      337 ----- 336
Oy      588 DIRRYETILEKAPFPTNYCILRLKLSHNMTRKRFKFWYEGKKNOSLOKIKRPLPYAA 647
Db      337 ----- 336
Oy      648 ICAHNFQYFDPSPDVAVFKSWERLSLNKNAETAILKATVSSCGELALGFFSCGFEF 707
Db      341 ----- 340
Oy      708 NDDDLAAGVDEDDLTKMLSKFTAOALRPYRFLSPARQEFLAGKRLIELLSDROEH 767
Db      341 ----- 340
Oy      768 QDLGLYHLMQISPMITVASAYNNFLNYSLSPTKAGPKIVSHLLLVNKKESLENISEN 827
Db      341 ----- 340
Oy      828 DQYLNKPEISLQMLKGLMQLCPQAVESVSEHLLVLAKTAVQSNVTAACSPFVLOF 887
Db      341 ----- 340
Oy      888 LOGRTLTGLNLQYFFDHPESLSLRSIHPRIRGNKTSPPAHFSVLETGDSQVPTID 947
Db      341 ----- 340
Oy      948 QDYASAFENWERNLAKEDONVKSNDQMRASPOLSTGYMKLSPKOYKIPCLEVDYN 1007
Db      341 ----- 340
Oy      1008 DIDVQGMLETILMTVFSASQRIELHLSNGFESTIRPALSELKASVTKCSISKLELSA 1067
Db      341 ----- 340
Oy      1068 ABOEILLTLPSLESLEVSGLTIOGODIFPRLDKFLCLKELSDLEGNINVSVPBEPFN 1127
Db      341 ----- 340
Oy      1128 FHHMEKLLIQISAEYDPSKLVKLQNSPRLHYFHLKCFSDFGSLMTMLVSGKRLTEIK 1187
Db      341 ----- 340
Oy      1187 VVKFQINFRHLNHFHLKCDPLFSLNCSLSMAVLAASCKRLRETE 381

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RESULT 2

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Oy      1188 FDSDFQAVPFAVSLPWFISLKLNLNEGQFPDEETSEKPAVILIGSLNUEELLPTGCG 1247
Db      382 FSGGCFEAMFVNILNPRFVSLKLNLKDDQFQDKETSEKPAQALGSLRLNEELLVPTGCG 441
Oy      1248 IYVAKLIIQCCQQLNLVLSPFFTLNDDSVYELAVAYLSGGFQKLENLKLSINKITE 1307
Db      442 IHOVAKLIVKQCLQCECLVLFVLFHDIDDDSVIATAAATSGGFOKLEMLDSMHKITE 501
Oy      1308 EGYRNFQALDMPMLQELDISRHFTECIAKQATVYKSLISQCVLRPLRLNMTSLLD 1367
Db      502 EGYRNFQALDMPMLQELDISRHFTECIAKQATVYKSLISQCVLRPLRLNMTSLLD 1367
Oy      1368 ADDIALNLVMEKRRIPQSKYTLTIQKYLPPSPIT 1401
Db      562 EEDMKVINDYKERHPOSKRLITLFWKLIVPSPVI 595

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AC Q9SEB8; PRELIMINARY; PRT; 589 AA.
 DT 01-MAR-2001 (TEMBLrel. 16, Created)
 DT 01-DEC-2001 (TEMBLrel. 16, Last sequence update)
 DE INHIBITOR OF APOPTOSIS PROTEIN 2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Crustacea; Vertebrata; Euteleostomi;
 OX Mammalia; Eulalia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RA Sequence from N.A.
 RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of
 RT Apoptosis Protein 1, 2, and 3 Genes."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: AF183431; AAG22971.1;
 DR HSP: Q13490; 108;
 DR InterPro: IPR001370; BIR.
 DR InterPro: IPR001315; Znf_Fing.
 DR Pfam: PF00653; BIR; 3
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00238; BIR; 3.
 DR SMART: SM00114; CARD; 1.
 DR PROSITE: PS01282; BIR_REPEAT_1; 1.
 DR PROSITE: PS0143; BIR_REPEAT_2; 3.
 DR PROSITE: PS0209; CARD; 1.
 KW Zinc-finger.
 SQ SEQUENCE: 589 AA; 66750 MM; B4F7089BD7CD285B CRC64;

Query Match

Best Local Similarity 6.78; Score 486; DB 11; Length 589;
 Matches 154; Conservative 75; Mismatches 186; Indels 138; Gaps 23;

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Oy      41 EOEKRAKMGQGYNSQSRSEAKRLKTEFTYDPRFMSWPOEMAAGFYHTGRLGVOCFCCSLTLFGN 167
Db      12 KENKE-KMKYDSC-----LYRMSYSAFPGVYVSRSLARAGFYVGNVKNXVC 62
Oy      98 FCCSLILFGAGLTRLPIEDHKKRPHDCCGFLNKKDVGNIATKADIVKVLKSLRGKRRYOEDEARLASFR 167
Db      63 FCCGLMDNMKQDPSPTKHNQFTYSCFVOTLISGGLQSAKASTSPAKSRHSLPLEQ 122
Oy      145 -----LKS-----LQCKMYR--OEDEARLASFRMPTVQGISPCVLSAG 185
Db      123 GGHSLSPNPLNSAAYDSFLRNPCSYAMSTEARLSTSMMP--LSPLSPALAKAG 180
Oy      186 FVETGKQDTPVQCFSCGCLGNMGGDDPMKEHAKMPKCEFLRSKSEETIYQISYK 245

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Db 181 FYYTGGDGVACFACGGKLSNNEPNDPLSEHRRHFPHCPELENTSEYORFS----- 232
Qy 246 FVDITGEHFNWVORELPMASAYCNDISIFAYEELRLDSFKDMPRESAVGAALAKAGLF 305
Db 233 -----VSNLSMQT-----HSARMSFLYWPSSVLVQPOLASAGRY 268
Qy 306 YTGINDIVOCFCGCGGLEKMOEGDDPLDHTRCFPCNPFLQNMKSSAEVTPDLOSR-GL 364
Db 269 YVDHNDVACFCGCGGLEKMOEGDDPLDHTRCFPCNPFLQNMKSSAEVTPDLOSR-GL 327
Qy 365 CELLETTSESINLEDSIAVGPVPEMAOGAOMFOEAKNLNEOLRAAYTSASFRHMSLDI 424
Db 328 LEQLLSTSDTSEEN--ADPPVYHLGPGE--NM--EDAVMMNTPVYKA----- 369
Qy 425 SSDLATDHLGCDLSIASKHISKPYOEPLVLEPEVGNLSVNCV-----EGEAG 473
Db 370 ----ALD--MGFSRSLVROTVOROI---LATGENTRTVSIDIYALLNADEREEREKQ 420
Qy 474 SCKTVLAKKIAFLAMSGCCPLLNRFOLVYLSLSTRPEGLASTICDOLLEKESYTEM 533
Db 421 SEET-----ASGDSLIRKNRMALFOOLTCVIP-----ILDDL--EASVLT 461
Qy 534 CERNIIQOLKNV 546
Db 462 EHDIIRO-KTOI 473

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RESULT 3

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ID 0902C6 PRELIMINARY: PRT: 589 AA.
AC 0902C6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE INHIBITOR OF APOPTOSIS PROTEIN 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Dong Z., Denton M., Gu S.M., Saikumar P., Venkatachalam M.A.;
RT Cloning of cDNA for rat inhibitor of apoptosis protein 2.;
RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF190020; AAF04585.1; -.
DR HSSP: Q13490; 10BH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; ZnF_ring.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
KW Zinc-finger.
SQ SEQUENCE 589 AA: 66777 MW: E6812FE3EA31142 CRC64:

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Query Match 6.7%; Score 486; DB 11; Length 589;
 Best Local Similarity 27.8%; Pred. No. 3e-26;
 Matches 154; Conservative 75; Mismatches 186; Indels 138; Gaps 23;

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Qy 41 EEOKERRAKMOKGYSOMSEAKRLKTFVYEEYSSWIP---OEMAAAGFTGVKSGIQC 97
Db 12 KKNKE--KKKYDFSCB-----LYRMSTYSAFPFGVPSSESLRAGGYTGVNDKVC 62
Qy 98 FCCSLILFGAGLTLRLPIEDHKRFRHPDCGF--LKNKDVGNIAKYDIRVKN----- 144

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Db 63 FCCGLIMDNMGKDGSPTEKHROFYPCSPFYQTLISGLQSAKKNTPSAKRRFANSLPQ 122
Qy 145 -----LKS-----LRGKMR--OEERARLASFNNPPYVIGISPCVLSENG 185
Db 123 GGIHSLPSNPLNSRAVEDFSLRMNPCTSYAMSTEEARFLSYGMW--LSFLSPAEELAKG 180
Qy 186 FVETGKODTVOCFCGCGGLEKMOEGDDPLDHTRCFPCNPFLQNMKSSAEVTPDLOSR-GL 245
Db 181 FYYTGGDGVACFACGGKLSNNEPNDPLSEHRRHFPHCPELENTSEYORFS----- 232
Qy 246 FVDITGEHFNWVORELPMASAYCNDISIFAYEELRLDSFKDMPRESAVGAALAKAGLF 305
Db 233 -----VSNLSMQT-----HSARMSFLYWPSSVLVQPOLASAGRY 268
Qy 306 YTGINDIVOCFCGCGGLEKMOEGDDPLDHTRCFPCNPFLQNMKSSAEVTPDLOSR-GL 364
Db 269 YVDHNDVACFCGCGGLEKMOEGDDPLDHTRCFPCNPFLQNMKSSAEVTPDLOSR-GL 327
Qy 365 CELLETTSESINLEDSIAVGPVPEMAOGAOMFOEAKNLNEOLRAAYTSASFRHMSLDI 424
Db 328 LEQLLSTSDTSEEN--ADPPVYHLGPGE--NM--EDAVMMNTPVYKA----- 369
Qy 425 SSDLATDHLGCDLSIASKHISKPYOEPLVLEPEVGNLSVNCV-----EGEAG 473
Db 370 ----ALD--MGFSRSLVROTVOROI---LATGENTRTVSIDIYALLNADEREEREKQ 420
Qy 474 SCKTVLAKKIAFLAMSGCCPLLNRFOLVYLSLSTRPEGLASTICDOLLEKESYTEM 533
Db 421 SEET-----ASGDSLIRKNRMALFOOLTCVIP-----ILDDL--EASVLT 461
Qy 534 CERNIIQOLKNV 546
Db 462 EHDIIRO-KTOI 473

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RESULT 4

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ID 09SE9 PRELIMINARY: PRT: 602 AA.
AC 09SE9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE INHIBITOR OF APOPTOSIS PROTEIN 1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT Cloning and Characterization of the Rat Homologs of the Inhibitor of
RT Apoptosis Protein 1, 2, and 3 Genes.;
RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AF183430; AAG22970.1; -.
DR HSSP: Q13490; 10BH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; ZnF_ring.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 1.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
KW Zinc-finger.
SQ SEQUENCE 602 AA: 67326 MW: CC91385E6A62DE5A CRC64:

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Db 458 MALFORLTSVLPILGSLLSAKVI 480

RESULT 6

ID 0921N0 PRELIMINARY; PRT: 374 AA.

AC 0921N0;

DT 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE SIMILAR TO BACULOVIRAL IAP REPEAT-CONTAINING 2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.

DR EMBL: BC011338; AAH1338.1; -

SEQ SEQUENCE 374 AA; 41915 MW; 1D2B54C32D7E46F3 CRC64;

Query Match 5.8%; Score 427.5; DB 11; Length 374;

Best Local Similarity 27.5%; Pred. No. 2.4e-22;

Matches 104; Conservative 49; Mismatches 138; Indels 87; Gaps 7;

QY 47 ARMQGYNS-----QMSAKRLKFTVYEPYSSWIP--QEMAAAGFTFGVKSIGIOCF 98

DB 9 ARLMSADFFELKDYDFSCELYRLS--TYSAPRGVYPSERSISLRAGFYTTGVNKKVCF 65

QY 99 CSSLIFGAGLRPLPIEDHKRPHPOGFLNKDVGNIAYDVRKNLKSRLGSKMRY-- 156

DB 66 CCGGLMDNKKOGSGPWEKHRLKLPSCNFVOTLNPNANSLASRPSPILSTAMSTMPISFAS 125

QY 157 -----QEEEARLASFRNMPFYVGIS 177

DB 126 SENTGFSGSYSPSPDPVNPFRANDCPALSTSPYHFAMNTEKARLLTYETWP--LSFLS 183

QY 178 PCVLEAGVFTGKQDTQVQFCGCGCLGWEGDDPKMKHAKWPRCELPKSKSEETT 237

DB 184 PAKLKAGFYIGPGDRAVACADGKLSMWERKDDAMSHORHPSCPPLKLGOS--- 239

QY 238 QYIOSYKGFVDITGEHFVNSWVQRELPMASAYCNDST-PAYEELRLDSFKDMPRESAVGV 296

DB 240 -----ASRTYVSNLSQTHAARTRTSNNPSSALVVS 271

QY 297 AALANAGLFTYTGIKDIVQFCGCGCLEKWOEGDDPLDHTRCFPPNCPFLONKSSAETVP 356

DB 272 OELASAGFYTGHSDDVKCFCCDGGGLRCWESGDDPWEHAKWPRCELYLRKIGQEFVSG 331

QY 357 DLOSNGELCELLETSES 374

DB 332 VQAGYPHLEQLLSTSDS 349

RESULT 7

ID 09E005 PRELIMINARY; PRT: 501 AA.

AC 09E005;

DT 01-MAR-2001 (Tremblrel. 16, Created)

DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE INHIBITOR OF APOPTOSIS PROTEIN 3.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN-MISTAR; TISSUE-OVARY;

RA Lareu R.R., Bradley C.K., Lacher M., Fris R.R., Dharmarajan A.M.;

RA "Cloning, characterization and regulation of an inhibitor of apoptosis

RT protein in the rat corpus luteum";

RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.

CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

DR EMBL: AF304333; AAG41192.1; -

DR HSSP: Q13490; 10BH.

DR InterPro: IPR001370; BIR.

DR InterPro: IPR001841; Znf_ring.

DR Pfam: PF00653; BIR; 3.

DR Pfam: PF00097; zf-C3HC4; 1.

DR SMART: SM00238; BIR; 3.

DR SMART: SM00184; RING; 1.

DR PROSITE: PS01282; BIR_REPEAT_1; 1.

DR PROSITE: PS0143; BIR_REPEAT_2; 3.

KN Zinc-finger.

SEQ SEQUENCE 501 AA; 56548 MW; 0973BFB28E81C5A0 CRC64;

Query Match 5.7%; Score 416.5; DB 11; Length 501;

Best Local Similarity 28.3%; Pred. No. 2.2e-21;

Matches 119; Conservative 60; Mismatches 162; Indels 79; Gaps 12;

QY 60 EAKRLKFTVYEPYSSWIPQEMAAAGFTFGVKSIGIOCFCSLLFGAGLRPLPIED--- 116

DB 26 EFNRLKTFANFPSSSPVSASTLARAGFLYTGGDTVQCFSCH-----AAVDHMOYGDNAV 80

QY 117 --HKRPHPCGFL-----LNKDVGNIAKYD 139

DB 81 GHRRLISPCRFITNGFYFNAGATOSTSPGIONGQYKSECVGNRNHFPALDRSETHADYL 140

QY 140 IR---VKNLSRLRGCKMRYOEEARLASFRNMPFYVGISPCVLEAGVFTGKQDTVQ 196

DB 141 LRTGGVVDISDTIYPRNPAMCSEEARLKTQNMPPYAH-LSPRELASAGLYTGGIDDOVQ 199

QY 197 CFSCGCGCLGNWEGDDPKMKHAKWPRCELPKSKSEETTQYIOSYKGFVDITGEHFVNS 256

DB 200 CFCGCGKRLNWEPCBRAWSEHRRHFPNCFVLAGN-----VAVRESGVS 244

QY 257 SWVQRELPMASAYCNDST-PAYEELRLDSFKDMPRESAVGVAAALAKAGLFTYTGKIDIVQCF 316

DB 245 S--DRNFPSTNSPRPMAAEVDARLYVTGTW--LTSYVKEQLARAGFALDEGDKVCF 300

QY 317 SCGCGCLEKWOEGDDPLDHTRCFPPNCPFLONKSSAETVPDLOSNGELCELLETSE--- 373

DB 301 HCGGGLADPKPSDDPWEQNAKWPYCGCKYLLDEGQ-ETYNINHLHLSLGEVYRFAEKTTP 359

QY 374 ----SNLEDSIANGPYIPEBAOGEAOWFOAKNLNEDLRALYTSASFRIHSLDDISSDLAT 430

DB 360 SVTKKIDITIFONPVQEAIRMGFNFKDKTKMWERKIQ---TSGS-NYLSLEVLIADLVS 415

RESULT 8

ID 09E004 PRELIMINARY; PRT: 501 AA.

AC 09E004;

DT 01-MAR-2001 (Tremblrel. 16, Created)

DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE INHIBITOR OF APOPTOSIS PROTEIN 3.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN-MISTAR; TISSUE-OVARY;

RA Lareu R.R., Bradley C.K., Lacher M., Fris R.R., Dharmarajan A.M.;

RA "Cloning, characterization and regulation of an inhibitor of apoptosis


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Db 30 ELYRSTSTFPVNPVSEERLARAAGYYTGVDVKCFSCGLVLDNMQPDNAMEKHKO 89
QY 120 FHPDGGFLN-----KDYGN----- 135
Db 90 YPSCSFVQNMNLISNLGLSTHSAPSLVANSLSLMSMTLSPSEEOGYGFSRSP 149
QY 136 -----AKYDIRVKNLSRLGKMRKRYOEERLARSFPNPFYOGISPCVLSAGFVF 188
Db 150 QDPVTRAEEDL--SHLSKSLNPSM--STEARLRTTHAMP--LMLFSLPTLAKAGLY 203
QY 189 TKGQDVOCFSCGCLGMEGDDDPKBEHAKWPCFELRSKSSSEITQYIYSYKGFVD 248
Db 204 LGTAKVACFTCGGSLNWEPEKDNAMSEHRHFPNCPFEVEN----- 244
QY 249 ITGEHFMVSWQRELPMASAYCNSISFAVELRLDSFKDMPRESAVGAALAKAGLYTG 308
Db 245 -----LMRDOP--SENVSWNTMOTHEARVKTFTIMPTRIPIVQPEQLADAGFYVG 292
QY 309 IKDIQVCFSCGCLGMEGDDPLDHTRCFP 340
Db 293 RMDVYKCFCCGGLRCMESGDDPMLEHAKWFP 324

RESULT 11
Q960U3 PRELIMINARY: PRT; 498 AA.
ID 0960U3
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE LD34777P.
GN IAP2.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Y, CN BW SP;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Flise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Pounenavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Gelinker S.;
RA Submitted (Aug-2001) to the EMBL/Genbank/DBJ databases.
RL EMBL: AY01844; AAK93268.1;
DR EMBL: AY01844; AAK93268.1;
SQ SEQUENCE 498 AA; 54537 MW; 0D0303DB2B26FA22 CRC64;

Query Match 4.6%; Score 336; DB 5; Length 498;
Best Local Similarity 27.8%; Pred. No. 1.3e-15;
Matches 98; Conservative 54; Mismatches 125; Indels 76; Gaps 13;

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QY 332 LDDHTRCFNCPFLONMKSASAVTPDLOSREGICELLFTTSNLEDSIANGP 384
Db 266 WEHAKWSKCFQVILLARGPAYVS-----EVLATTA-ANASSOPATAP 307

RESULT 12
Q09123 PRELIMINARY: PRT; 87 AA.
ID 009123
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 1C (NEUONML APOPTOSIS
DE INHIBITOR PROTEIN, RELATED SEQUENCE 5) (FRAGMENT).
DE BIR1C OR NAIP3 OR NAIP-RS3.
GN BIR1C OR NAIP3 OR NAIP-RS3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-129/SVJ;
RX MEDLINE-97131520; PubMed-8975718;
RA Scharf J.M., Damron D., Fritsella A., Bruno S., Beggs A.H.,
RA Kunkel L.M., Dietrich W.F.;
RT "The mouse region syntenic for human spinal muscular atrophy lies
RT within the lgnt critical interval and contains multiple copies of Naip
RT exon 5."
RL Genomics 38:405-417(1996).
CC -1 SIMILARITY: CONTAINS 1 BIR DOMAIN (BACULOVIRAL INHIBITION OF
CC APOPTOSIS PROTEIN REPEAT).
DR EMBL: U66328; AAC52976.1;
DR HSSP: Q13490; 108H.
DR MGD: MGI:1298225; Birc1c.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR; 1.
DR SMART: SM00238; BIR; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; PARTIAL.
DR PROSITE: PS01443; BIR_REPEAT_2; 1.
FT NON_TER 1
FT TER 87
SQ SEQUENCE 87 AA; 9997 MW; B184943B3BC52E3A CRC64;

Query Match 4.4%; Score 325; DB 11; Length 87;
Best Local Similarity 70.1%; Pred. No. 5.7e-16;
Matches 61; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

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RC STRAIN-BRED LECHORN; TISSUE=SPLEEN;
RX MEDLINE-21158006; PubMed-11261557;
RA Zhou H., Liu W., Lamont S.J.;
RT "Genetic variation among chicken lines and mammalian species in
RT specific genes";
RL Poul. Sci. 80:284-288(2001).
DR EMBL; AF221082; AAF5319.1; -.
DR HSSP; Q13490; IOBH.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 2.
FT NON_TER 1 1
FT 195 195
SQ SEQUENCE 195 AA; 22347 MW; 9C39BFA755E24E48 CRC64;

Query Match 4.4%; Score 323.5; DB 13; Length 195;
Best Local Similarity 35.1%; Pred. No. 2.4e-15;
Matches 72; Conservative 29; Mismatches 63; Indels 41; Gaps 7;

OY 46 RAKQKGYNSQMSSEARLKTFTYEPYSSWIRQEMAAAGFTYGVKSGIQCCCSLILF 105
DB 19 RSKL---HNSMSTEARLRTFHAM-PLMFLSPALAKAGLYLGTADKACFTC----- 69
OY 106 GAGLTRLPDIED-----HKRPHDCGFLNK-----DVCNIAKYDIRVKNLKSRLRGK 153
DB 70 GGQLSNWEPRDNMSEHRRHFPNCPFEVNLMDQPSFNNSNV----- 112
OY 154 MRQEEARLASFRNMPFYVGISPCVLSAGCFVFTGKDTVOCFSCGGLGMWEGDDP 213
DB 113 --MOTHEARVKTFTINWTRIP-VOPQLADAGFYVGRNDVVCFCDDGLRCMESGDDP 169
OY 214 WKEHAKWPCPCFLRSKSSSEITQ 238
DB 170 WIEHAKWPCPCFLRVKKGGEFVSQ 194

RESULT 14
O91A69 PRELIMINARY; PRT; 197 AA.
ID O91A69;
AC O91A69;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE INHIBITOR OF APOPTOSIS 1 (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRED FAYOUMI; TISSUE=SPLEEN;
RX MEDLINE-21158006; PubMed-11261557;
RA Zhou H., Liu W., Lamont S.J.;
RT "Genetic variation among chicken lines and mammalian species in
RT specific genes";
RL Poul. Sci. 80:284-288(2001).
DR EMBL; AF221083; AAF3320.1; -.
DR HSSP; Q13490; IOBH.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 2.
FT NON_TER 1 1
FT 197 197
SQ SEQUENCE 197 AA; 22602 MW; D7923DABCF623E1A CRC64;

Query Match 4.4%; Score 323.5; DB 13; Length 197;

Best Local Similarity 35.1%; Pred. No. 2.5e-15;
Matches 72; Conservative 29; Mismatches 63; Indels 41; Gaps 7;
OY 46 RAKQKGYNSQMSSEARLKTFTYEPYSSWIRQEMAAAGFTYGVKSGIQCCCSLILF 105
DB 20 RSKL---HNSMSTEARLRTFHAM-PLMFLSPALAKAGLYLGTADKACFTC----- 70
OY 106 GAGLTRLPDIED-----HKRPHDCGFLNK-----DVCNIAKYDIRVKNLKSRLRGK 153
DB 71 GGQLSNWEPRDNMSEHRRHFPNCPFEVNLMDQPSFNNSNV----- 113
OY 154 MRQEEARLASFRNMPFYVGISPCVLSAGCFVFTGKDTVOCFSCGGLGMWEGDDP 213
DB 114 --MOTHEARVKTFTINWTRIP-VOPQLADAGFYVGRNDVVCFCDDGLRCMESGDDP 170
OY 214 WKEHAKWPCPCFLRSKSSSEITQ 238
DB 171 WIEHAKWPCPCFLRVKKGGEFVSQ 195

RESULT 15
O09119 PRELIMINARY; PRT; 87 AA.
ID O09119;
AC O09119;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE NEURONAL APOPTOSIS INHIBITORY PROTEIN RELATED SEQUENCE 1
DE (FRAGMENT).
GN BIRC1-RS1 OR NAIP-RS1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE-97131520; PubMed-8975718;
RA Scharf J.M., Damron D., Fritsella A., Bruno S., Beggs A.H.,
RA Kunkel L.M., Dietrich W.F.;
RT The mouse region syntenic for human spinal muscular atrophy lies
RT within the 1q11 critical interval and contains multiple copies of Naip
RT exon 5.";
RL Genomics 38:405-417(1996).
DR EMBL; U66324; AAC52972.1; -.
DR HSSP; Q13490; IOBH.
DR MGP; MGI:109439; Birc1-rs1.
DR InterPro; IPR001370; BIR.
DR Pfam; PF00653; BIR; 1.
DR SMART; SM00238; BIR; 1.
DR PROSITE; PS0143; BIR_REPEAT_2; 1.
FT NON_TER 1 1
FT 87 87
SQ SEQUENCE 87 AA; 9958 MW; E601604230BCID25 CRC64;

Query Match 4.4%; Score 320; DB 11; Length 87;
Best Local Similarity 69.0%; Pred. No. 1.3e-15;
Matches 60; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

OY 82 AAAGFTYGVKSGIQCCCSLILFAGAGLTRLPDIEDHKRPHDCGFLNKDVGNIAKYDIR 141
DB 1 AAAGFTYGVKSGIQCCCSLILFSTRLRKLPDENHKKLRCECFDQKDVGNIGKAKDIR 60
OY 142 VKNLKSRLRGKMRQEEARLASFRN 168
DB 61 VKSPKMLRGKARTHEEARLESFED 87

Search completed: September 30, 2002, 15:06:30
Job time: 186 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 30, 2002, 14:59:19 : Search time 41.9 Seconds
(without alignments)
3719.249 Million cell updates/sec

Title: US-09-830-338-1

Perfect score: 7308

Sequence: 1 MAQQKASDERISQFDHNL.....SKYLLIKKWLFPSPILQK 1403

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7308	100.0	1403	18	AAW20032
2	7308	100.0	1403	20	AA114075
3	7308	100.0	1403	21	AA109539
4	7308	100.0	1403	21	AA108053
5	7284	99.7	1403	18	AAW20033
6	6691	91.6	1295	20	AA114080
7	6691	91.6	1295	20	AA109540
8	6373.5	87.2	1232	17	AA108217
9	661	9.0	1204	22	AA102881
10	654	8.9	1070	22	AA102881
11	653	8.9	1024	22	AA102880

12	566	7.7	841	22	AAW23595
13	545.5	7.5	118	21	AAW53493
14	536.5	7.3	738	22	AAW67526
15	462	6.3	618	18	AAW19746
16	462	6.3	618	18	AAW19583
17	462	6.3	618	18	AAW13545
18	462	6.3	618	19	AAW69296
19	462	6.3	618	20	AAW33998
20	457.5	6.3	612	18	AAW13555
21	457.5	6.3	612	19	AAW69299
22	441.5	6.0	591	18	AAW19586
23	440	6.0	600	19	AAW69298
24	437.5	6.0	496	18	AAW19584
25	437.5	6.0	496	19	AAW69297
26	436.5	6.0	604	18	AAW19747
27	436.5	6.0	604	18	AAW13546
28	436.5	6.0	604	20	AAW32703
29	436.5	6.0	604	20	AAW33997
30	435	6.0	1141	22	AAW50694
31	431.5	5.9	496	18	AAW19745
32	431.5	5.9	604	18	AAW19582
33	431.5	5.9	604	19	AAW69295
34	427.5	5.8	602	18	AAW19585
35	407	5.6	497	21	AAW59451
36	403	5.5	497	18	AAW19581
37	403	5.5	497	19	AAW69294
38	403	5.5	497	21	AAW59985
39	354	4.8	642	22	AAW25640
40	340.5	4.7	438	17	AAW04583
41	336	4.6	498	22	AAW62863
42	335	4.6	498	18	AAW19748
43	320	4.4	60	21	AAW01849
44	318.5	4.4	306	22	AAW02925
45	304.5	4.2	438	22	AAW48191

ALIGNMENTS

RESULT 1	
AAW20032	
ID	AAW20032 standard; Protein: 1403 AA.
AC	AAW20032;
DT	06-OCT-1997 (first entry)
DE	Neuronal apoptosis inhibitor protein (NAIP).
KW	Neuronal apoptosis inhibitor protein; NAIP; diagnosis: therapy; cancer; AIDS; amyotrophic lateral sclerosis; spinal muscular atrophy.
KW	spinal muscular atrophy.
OS	Home sapiens.
PN	W09726331-A2.
PD	24-JUL-1997.
PF	17-JAN-1997; 97WO-IB00142.
PR	19-JAN-1996; 96GB-0001108.
PA	(UYOT-) UNIV OTTAWA.
PI	Korneluk RG, Mackenzie AE, Robertson G, Roy N, Tamai K; WPI: 1997-385335/35.
DR	N-PSDB: AAT71265.
PT	New neuronal inhibitor of apoptosis - useful for diagnosing and treating, e.g. cancer, AIDS or amyotrophic lateral sclerosis
XX	

PS Claim 41; Fig 6A-I; 102pp; English.
XX
CC Novel human neuronal apoptosis inhibitor protein (AAM20032), or NAIP,
CC is a negative regulator of apoptosis, partic. neuronal apoptosis
CC and, when deficient or absent, contributes to neurodegenerative
CC phenotypes such as spinal muscular atrophy (SMA) and amyotrophic
CC lateral sclerosis. Its amino acid sequence was deduced from a
CC cDNA clone (AAT71265) obt. from a human foetal spinal cord cDNA
CC library. NAIP polypeptides, esp. those containing at least two
CC BIR (baculovirus iAP repeat) domains, can be expressed in host
CC vector systems and used to increase or induce apoptosis in host
CC treatment of AIDS, neurodegenerative disease, myelodysplastic
CC syndromes or ischaemic injury, to screen for (anti)agonists, or to
CC produce antibodies useful for inhibiting apoptosis.
XX
SO Sequence 1403 AA;

Query Match 100.0%; Score 7308; DB 18; Length 1403;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MATQQAASDERISQFDHNLPELSALLGLDAVOLAKELPEEPOKRAKQKYNQMSHSE	60
DB	1	maeqqkaderlsqfchllpelsallgldavqlakelpeeqkerakmqgynsqmrse	60
QY	61	AKRLKFTVYBPPSSWIPQEMAAAGFTGVSGIGCCSLILEGAGLTRLPTEDHKRF	120
DB	61	akrlkfvcyepyswlpemaaaglyfgyvsgigccfcsallfagagltrlpiedhkrf	120
QY	121	HPDCGFLKKDVGNIAKTDIRKVNLSRLKGMKRYQEEEARLKSFRMMPYVGISPCV	180
DB	121	hpcdglflnkdvgnlaktdirvknlsrllrgkmrygeearlsfrmplyvgispcv	180
QY	181	LSEAGVFETKQDVTQCCSGCGCLNMEEGDDPKWEAKKPPKCEFLRSKSSSEITQYI	240
DB	181	lseagvfetkqdvtyqccsgcgclnmeeegddpkweakppkceflrskssseitqyi	240
QY	241	OSYKGFVDITGHEFVNSVQRELPMAAAYVNDISFAYEELRLDSFKMMPRESAVGVALA	300
DB	241	osykgfvdtghefvnsvqrelpmaaaayndisfayeelrldsfkmpresavgvala	300
QY	301	KAGLFYTGIRKDIYVCFSCGCGCLEKMOEGDDPLDHTRCFNCPLONMSSAETVPLDLS	360
DB	301	kaglfytgikrdiyvcfscgcgclekmoegddpldhtrcfncpflonmssaeavpldls	360
QY	361	RGEICELLETTSBSNLEDSIAVGPIVPEMAQCEAQMFOEAKNLEQLRAAYTSASRRHS	420
DB	361	rgelcellettsesnledsiavgpivpemaqceaqmfgeeknlneqlraaytsasrrhs	420
QY	421	LIDSISPLATDHLGCDLSIAASKHISKPVQDEPLVLPDVFGNTLSVNCVCEAGSGKTVLL	480
DB	421	lidsispladchllgcdlsiaskhlskpvqdeplvlpdvfgnlsvncvceagsgkvtll	480
QY	481	KKIAFLWASCCCPILNRFOLVFLYLSSTRPDEGLASTICDOLLEKESGYTMCKRANITQ	540
DB	481	kkiatlwascgcpilnrfolyflsstrpdeglasticdolleksgytmckranitq	540
QY	541	QLKNQVLEFLDDVKEICSPVOYIGKILQKNHLSRTCLLIATVTRNARDIRYLETILEIK	600
DB	541	qlknqvlflldvkeicspvoygkilkqknhlsrtclliatvtrnardiryletileik	600
QY	601	APFFYTVICILKRLFSHNTRLRKFFVYGGKQNSLOKTOKTPLFVAALCAAMFQPEDPS	660
DB	601	apffytvcilrkrlfshnttrlrkffvfygkngslqkqrpilvaalcaahfaypfdps	660
QY	661	FDDVAVFKSYMERLSLRNKATAEILKATVSSGGLALKGFFSCFFENDDDLAAGVDED	720
DB	661	fdavavfksymerslsrlnkataelilkatvssgglalkgffscfendddlaagvded	720
QY	721	EDLTCNLMSKFTAQRLPFYRFLSPAPQELAGRLITELDSDQEQHDLCLYLHKLQINS	780
DB	721	edltcmclmskfraqrlrpfyrfliapaqelagrlitelddsqeqhdlclylhklqins	780

QY	781	PMKTVSAVNNFLNYSLSPTKAGPKIVSHLLHVDNKSESLENTSEDDYDLKHQPEISLQ	840
DB	781	pmtvsaavnflnysslsptkagpkivshllhvdnkseleentseddydlkhqpelislq	840
QY	841	MOLLRLGILQICPOAYFVSWSHLLVLAIKTAYGNTVAACSPVLOFLQGRITLLGALNL	900
DB	841	mllrlglilqicpoyfvswwshllvlaiktaygntvaacspvlylqgritllgalnl	900
QY	901	QYFDPHEPSLILRSIRHPITRGNTSPRAHFSVLETCFDSQVPTDOYASAFEMENEM	960
DB	901	qyfdhpeslilsirhprtgntsprahfsvleetcfdsqvptdoyasafememenem	960
QY	961	ERNLAEEKDANKSYMDOGRASPDLSGTWKLSPKQKIPCLLEVNDIDVYGOMLLET	1020
DB	961	ernlaekednksymdoqraspdlstgwklspkqkipcllevndidvvgomllet	1020
QY	1021	MTVFSASQRIELHNLNISRPFESIRPALIELSKASVTKCSIKLELSAEOELLTLPSE	1080
DB	1021	mtvfasqrlelhnlnsrpfesirpalieleksasvtkcsiklelsaeeolltlpse	1080
QY	1081	SLEVSQTIOSODQIFPNLDKFLCLKELSVDEGNTNVESVIPEEPNPFHMEKLLIOISA	1140
DB	1081	slevsqtiqqdqiifpnldkflclkelsvdlegntnvesvipeeppnfhmecllioisa	1140
QY	1141	EYDPSKLVKLIONSPLHVPFLKCNFFSDFGSLMTLVSCKLTETIKRSDSPQAVPVA	1200
DB	1141	eydpskvlvklionsplhvpflkcnffsdfgslmtlvscckltetiksdsdpqavpva	1200
QY	1201	SLPNEFSILTLNLEGGQPDDETSERKFAVILGSLSNLEELLPTGSGTYRVAKLIIQCC	1260
DB	1201	slpnfsltlnlleqqpddetserkfavilgslsnleellptgsgtyrvakliiqcc	1260
QY	1261	QLHCLRVLSFFETLNDSDVEIAKVAISGFOKLENTKLSINHITTEGVRNFEQALDNM	1320
DB	1261	qlhclrvlsffetlndsdveiakvaisgfoklenklsinhittegvrnfeqaldnm	1320
QY	1321	PMLQELDISRHPTECIRKQATTVKSISQCVLRRLRLNKLWSLWDADDTALLNWKER	1380
DB	1321	pmlqeldisrhptecirkqatvksisqcvlrrlrlnklwslwdadtdallnwker	1380
QY	1381	HPQSKYTLTLLQKWLIPSPRIQK 1403	
DB	1381	hpqskyltllqkwlipspriqk 1403	

RESULT 2
AAV14079
ID AAV14079 standard; Protein: 1403 AA.
AC AAV14079:
DT 20-JUL-1999 (first entry)
DE Genadotropic hormone protein sequence.
DE Genadotropic hormone protein sequence.
DE Genadotropic hormone; excessive ovulation animal; transgenic animal;
KW Gonadotropic cell; somatic cell chromosome.
OS Homo sapiens.
XX JP11113444-A.
XX
XX PD 27-APR-1999.
XX
XX PF 14-OCT-1997; 97JP-0280830.
XX
XX PR 14-OCT-1997; 97JP-0280830.
XX
XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX (SAKA-) SAKAI H.
XX
XX DR WPI: 1999-320709/27.

DR N-PSDB: AAX58000.

XX An excessive ovulation animal - useful for improving the
PT productivity of animals
XX

PS Claim 3: Page 11-14; 18pp; Japanese.

XX This sequence represents a gonadotropic hormone.
CC The invention relates to an excessive ovulation animal, which is a
CC transgenic animal with a totipotent cell containing a DNA fragment
CC containing a promoter sequence and a gonadotropic hormone coding
CC sequence. The DNA fragment is in the somatic cell chromosome. The
CC excessive ovulation animal is useful for improving the productivity of
CC animals. The method can improve the productivity of a useful animal.
XX

SO Sequence 1403 AA;

Query Match 100.0%; Score 7308; DB 20; Length 1403;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NATQKASDERISQPDHMLPELSALLGLDAVQLAKELEEDQKERAKKQKQNSQMRSE 60
DB 1 matqkaaderisqfdhmlpelisallglдавqakeleeeeqkerakmqkqnsqmrse 60
QY AKRLKFTYTPYEPYSSWIFQENAAAGFYTFGVASGIQCCSLILRGAGITRLPIEDHKRF 120
DB AKRLKFTYEPYSSWIFQENAAAGFYTFGVASGIQCCSLILRGAGITRLPIEDHKRF 120
QY 61 AKRLKFTYTPYEPYSSWIFQENAAAGFYTFGVASGIQCCSLILRGAGITRLPIEDHKRF 120
DB 61 AKRLKFTYEPYSSWIFQENAAAGFYTFGVASGIQCCSLILRGAGITRLPIEDHKRF 120
QY 121 HPDGFELINKDYNIAKDYIRVKNLKSRLRGKMRYOEEEARLARSBRMPFYVOGISPCV 180
DB 121 hpdgfillinkdvnakdyirvknlsrlrgkmrygeeeearlasbrmpfyvqgispcv 180
QY 181 LSEAGFVFTGKODTVQCFSCGCGCGLGNWEEGDPMKEHAKWPKCFELRSKSSSEETIYXI 240
DB 181 lseagfvftgkdtdvqcfscgcgclgnweegddpmkehakwfkcelrlsksseetiyyi 240
QY 241 OSYKFFVDTGHRFNYSWQRELPMASAYCNDSTFAYEELRLDSRKDWREBNAVGAALIA 300
DB 241 qsykffvdtghefnyswqrelpmasaycndstfayeelrldsrdkdwrebnavgaaia 300
QY 301 KAGLFYTGIDKIDVQCFSCGCGCGLGNWEEGDPMKEHAKWPKCFELRSKSSSEETIYXI 360
DB 301 kaglfytgikdvdvqcfscgcgclgnweegddpmkehakwfkcelrlsksseetiyyi 360
QY 361 KGLIFYTGIDKIDVQCFSCGCGCGLGNWEEGDPMKEHAKWPKCFELRSKSSSEETIYXI 360
DB 361 kglifytgikdvdvqcfscgcgclgnweegddpmkehakwfkcelrlsksseetiyyi 360
QY 361 KGLIFYTGIDKIDVQCFSCGCGCGLGNWEEGDPMKEHAKWPKCFELRSKSSSEETIYXI 360
DB 361 kglifytgikdvdvqcfscgcgclgnweegddpmkehakwfkcelrlsksseetiyyi 360
QY 421 LIDISSDLATDHLGCDLSIAKSHISKPYQEBLVLPYVNGINNSVYCVGEAGSGKTIVL 480
DB 421 lidsdlatdhlhgcdlsiakshiskpyqeblvlpvnginnsyvcvgeagsgktivl 480
QY 481 KKIATFLASGCCPLNRFOLVYLSLSSTRPDEGLASIIDCDLLEKESGVTMCAMNITIQ 540
DB 481 kkiatflasgccplnrfolvylslsstrpdeglasiidcdllekesgvtemcnitiq 540
QY 541 QLNKOVLELLDDYKEICSTPOVIGKLIQKNHLSRTCLLIAVBTNRADIRRYLETILEIK 600
DB 541 qlknovlellddykeicstpovigkqliqknhlsrtclliavbtrardirryletileik 600
QY 601 APEFYNTWCILBKLSHNNTRLRKFMVYFGKNOSIQIKTKTFLFAALCAHMFQYRFDPS 660
DB 601 apefyntwcilbklsnntrlrkfmvyfgknosiqiktktflfaalcahmfqyrfdps 660
QY 661 FDDVAVFKSYMERLSLRNKATAEILKATVSSCGELALKGFSCCFEENDDLAEGVDED 720
DB 661 fddvavfksymerlslnrkataeilkatvsscgelaikgfsccefenddlaeagvded 720
QY 721 EDLTNCLMSKFTAQRLRPYRFLSPAFOEFLAGMRLIELLSDROEHODLGLYHLKQINS 780
DB 721 edltnclmskftaqrlrpyrflspafogeflagmrlieellsdroehodlgllyhlkqins 780

QY 781 PMMTVASAVNNFLNVYSSLPSTKAGPKIVSHLHLVDNKNESLENISENDYTLKHOPEISIQ 840
DB 781 pmmtvassavnnflnvyslpsstkagpkivshllhvdnksenlenisendytlkhppeisiq 840
QY 841 MOLLGLMOICPOAFYSWSEHLVLAATKATAYQNTVAACSPFVQFLOGRTLTGALNL 900
DB 841 mllglmoicpofyswsehlvlatkatayqntvaacspfvlqflogrtltgalnl 900
QY 901 QYFDPHPSLSLRISIHPIRGKNTSPRAHFSVLETCFDKSOVPTIDODYASAFPMHNEW 960
DB 901 qyfdphpslslrishpircgkntsprahfsvletcfdksovpitidodyasafpmhnew 960
QY 961 ENILAEKEDNVASYMDKMRASPDLSGTGKLSPPQYKIRPCLEVVYNDIDVYGOMLETL 1020
DB 961 enilaekednvasymdkmraspdlsgtgklsppqykrpclevvnyndidvygomletl 1020
QY 1021 MTFVASORIEHLNHSRGFIESIRPALELSKASVYKCSISKLELSAAEQELLTLPSLE 1080
DB 1021 mtfvasorielhlnhsrgfiesirpalelskasvycsksklelsaaeqelltlpsle 1080
QY 1081 SLEVSQGTIQSDQIFPNLDKFLCLKELSVDEGNINVSIVIDEFPNPHMEKLLIQISA 1140
DB 1081 slevsqgtiqsdqifpnldkflclkelsvdegninvsividefpnphmeklliqisa 1140
QY 1141 EYDPSKIVKLIQNSPMLAHFHLKCNFSDPGSLMMLVSCKRLTEIKFSDFSFOAVPFA 1200
DB 1141 eydpskivkliqnsplahfhlkcnfsdpgslmmlvscckrlteikfsdfsfoavpfa 1200
QY 1201 SLPNFSLKILNDEGQFPDEETSEKFAVTLISLSNLEELIPTDGIYRVAKLLIQOQO 1260
DB 1201 slpnfslkilndeegqfpdeetsekfavtlislsnleeliptdgiyrvaklliqoqo 1260
QY 1261 QHLCLRVLSFFRTLNDOSVVEIAKVAISGFOKLEMLKISINHKTITEBQYRNFPQALDMA 1320
DB 1261 qhlclrvlsffrtlndosvveiakvaisgfoklemlkisinhkitebqyrnfqaldma 1320
QY 1321 PNLGELDSRHFTFECIKAAQNTVKSLSOCVLRPLRLINMISWLLDADIDLLVMYKER 1380
DB 1321 pnlgeldsrhftfecikaqntvkslsocvlrplrlinmismwlldadidllvmker 1380
QY 1381 HPQSKYLTITLQKMLLPFSPIQK 1403
DB 1381 hpqskyltitlqkmlpfspliqk 1403

RESULT 3
AAV09539
ID AAV09539 standard; Protein; 1403 AA.
XX
AC AAV09539;
XX
DT 20-JUL-1999 (first entry)
XX
DE Human apoptosis inhibiting protein #1.
XX
KW Human; apoptosis inhibitory protein; apoptotic disease; diagnosis;
KW spinal muscular atrophy.
XX
OS Homo sapiens.
XX
PN JP11116599-A.
XX
PD 27-APR-1999.
XX
PF 14-OCT-1997; 97JP-0280831.
XX
PR 14-OCT-1997; 97JP-0280831.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
WI PI; 1999-323531/27.
DR N-PSDB: AAX56272.

XX New Apoptosis Inhibitory protein - useful for determining mechanism
 PT of various apoptotic diseases e.g. human spinal muscular atrophy
 XX
 PS Claim 1; Page 4-8; 16pp; Japanese.
 XX
 CC The present sequence represents a human apoptosis inhibitory protein.
 CC The apoptosis inhibitory protein is useful for the elucidation of
 CC the mechanism of various apoptotic diseases such as human spinal
 CC muscular atrophy and the diagnosis, the prevention and the treatment
 CC of such diseases.
 XX
 SO Sequence 1403 AA:

Query Match 100.0%; Score 7308; DB 20; Length 1403;
 Best Local Similarity 100.0%; Prod. No. 0;
 Matches 1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MATQKASDERISQFDHNLPELSALIGDAVQALAKELSEERQERAKMOGYSQMRSE 60
 1 mdtqkaederisqfdhnlpeelsaligdavqalakelseeqkerakmqkyasqmrse 60
 61 ARRLTFYVYBPYSSWIOBMAAGFYTWGKSGIQGCSLIFGAGLTRLEIEDHKRF 120
 61 arrltfvyvbysswioebmaagfytwgksgiqgcsllifgagltrleiedhkrf 120
 121 HPDCCFLNKDVGNIAKADIRKMLKSRGKRWYQEEERARLASRRNMPFYVQGISPCV 180
 121 hpdccflnkdvgniakadirkmlksrgkwrwyqeeerarlasrrnmpfyvqgispcv 180
 181 LSEAGFVPTGKODTVQCGCGCCGCMWEGDDPMKEMHAKMPCCEFLRKRSSEETIOTY 240
 181 lseagfvptgkodtvqcgcgccgcmwegddpmkemhakmpcceflrkrsseetioty 240
 241 QSYKGFVDITGEHFVNSWVQRELPMAAYCNISIFAYEELRLDSRKDPRESAVGVALA 300
 241 qsykgfvdtigehfvnswvqrelpmaycnsifayeelrldsrdkrdpresavgvala 300
 301 KACLFYTGIDIVQCSGCCGCEKQWEGDDPLDHTRCFPNCPFLQNNKSSAEVTPLOS 360
 301 kaclfygtgidivqcsgccgcekwegddpldhtrcfpncpflqnnkssaevtplos 360
 361 RGLCELLETTSESNLEDSIAVPIVPMAGQEWQEOANLNBOULRAAYTSASFRHMS 420
 361 rglcelletteesnledsiavpivpmagqewqeoanlnboulraaytsasfrhms 420
 421 LDISSDATDHLGCDISASKHISKRVQEPVLPVFGNLNSVMCVEGEASGKTVLL 480
 421 ldisssdatdhlgcdisaskhiskrvqepvlpvfgnlnsvmcvegeasgktvll 480
 481 KRIATLMSGCCPLLNRPOLVFLYLSSTPRDEGLASITCDOLLEKESVTEKMRNIIQ 540
 481 kriaflmsgccpllnrpolvflylsstprdeglasitcdollekesvtekmrniiq 540
 541 QLANQVFLLDYKELCSIFQVIGKLIQKNHLSRTCLLAVRTNARIDIRYLETILEK 600
 541 qlanqvflldykelsifqvigkqliqknhlsrtcllavrtnaridiryletilek 600
 601 AEPFYNTVCLTRKLFSGHNTRLRKRFNVYFGKQNSLOKTOKPLFPAALCAHWQYPPDPS 660
 601 aepfyntvcltrklfsghntrlrkrfnvyfgkqnsloktokplfpaalcahwqyppdps 660
 661 FDDVAVFKSYMERLISRNKATAEILKATVSSGELALKGFSGCCFERNDODLAEGVDED 720
 661 fddvavfksymerliskataeailkatvssgelalkgfsgccferndodlaegvded 720
 721 EDLJNOLMSKFLAORLPRPYRFLSPAFQEFLAGRLTELLDSQDQEHODGLYHLQIOMS 780
 721 edljnolmskflaorlprpyrflspafqeflagrltelldsqdqehodglyhlqioms 780
 781 PMMTVSAYNNFLNYSVSPSTKAGPKTVSHLHLVDNKESLENISENDYLRKHQPEISIQ 840
 781 pmtvsaynnflnysvspstkagpktvshlhlvdnkeshlenisendylrkhppeisio 840

Db 781 pmmtvsaynnflnysvspstkagpkivshllhldvdkeshlenisenddykhppeisio 840
 QY 841 MQLRLGMOICPOAYFSWVSEHLVYALTKTAVQSNVMAACSPVLOFLQGRFTLTGALNT 900
 841 mqlrlgmoicpoyfswvsehllvyaltktavqsnvmaacspvlyoflqgrftltgalnt 900
 901 QYFDPBESLSLRSIHPIRGNKTSPPRAHFSVLETCEDKNSQVPTIYODYASAFEPNMEW 960
 901 qyfdpbeslsllsrhpiirgnktspprahfsvleetcdknsqvptiyodyasafepnme 960
 961 ERNLAKEEDNVASVYDMQRRASPDLSGVMKLSPOYKIFCTLEVDVNDIDVYQDMLETL 1020
 961 ernlakeednvsvydmqrraspsdlsqvmklspsykykfctlevdvndidvyqdmle 1020
 1021 MTFVSASQRIEHLNHSRGFESTIRPALLESKASVYKCSISKLSAARDQLLTPSLLE 1080
 1021 mtfvsasqriehlhnsrgfestirpalleskasvykcsisklsaarqlltpslle 1080
 1081 SLEVSGTIOGSDOIFPNLXKFLCLKELSYDLEGNINVFSVIPEEPNFMHMKLTIOTISA 1140
 1081 slevsgtiogsdofpnlxkflclkelisydlegninvfsvipeepnfmmhmkltiotisa 1140
 1141 EYDPSKLVKLIQNSPMLHVFHLKCNFSDFGSLMTMLVSCKLTLEKSDSFFQAVPEVA 1200
 1141 eydpsklvklignspmlhvfhlkcnfsgdsgslmtmlvsccktletkssdsffqavpe 1200
 1201 SLPNFISLKLINLEGOFPDEETSEKFAVILGSLSNLEBELLPICDGYRVAKLIIQCCQ 1260
 1201 slpnfislklilnlegofpdeetsekfavilgslsnlebelipicdgyrvakliiqccq 1260
 1261 QLNCCLAVLSFEFTLNDOSVEIAKVAISGFOKLENLKLSINHRTDEGRANFPQALDNM 1320
 1261 qlncclavlsfeftlndosveiakvaisgfoklenlksinhrtdegranfpqaldnm 1320
 1321 PMLOBLDSRHFTPECIRKQATTVKSLSCVRLRLRLNMLSWLADADIALANMKER 1380
 1321 pmlobldsrhftpecirkqatvkslscvrlrlrlnmlswladadialanmker 1380
 1381 HPOSKYVLTILQKWLIPESPIIQ 1403
 1381 hpkskyvltlqkwllpesspiiq 1403

RESULT 4
 AAY88053
 ID AAY88053 standard; Protein: 1403 AA.
 AC AAY88053;
 DT 22-SEP-2000 (first entry)
 DE Human NAIP protein.
 XX
 KW NAIP; apoptosis inhibiting protein; monoclonal antibody; diagnosis;
 KW apoptosis disease onset mechanism; drugs development; prevention;
 KW treatment; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 256..586
 FT Region /note="Immunogenic region, specifically described
 FT Region 841..1052 in Claim 1"
 FT /note="Immunogenic region, specifically described
 FT in Claim 1"
 PN W0200024889-A1.
 XX
 PD 04-MAY-2000.
 XX
 PF 22-OCT-1999; 99WO-JP05841.
 XX

PR 26-OCT-1998; 98JP-0304550.
XX
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA (SAKA/) SAKAI H.
XX
XX Sakai H, Ikeda J;
PI
XX MPI: 2000-350731/30.
DR N-PSDB; AAA39808.
XX
PT Simple and accurate quantitation of human apoptosis inhibitory protein
PT (NAIP) with monoclonal antibodies, for disease diagnosis and
PT development of drugs to prevent and treat apoptosis-related diseases
XX
XX Claim 1; Page 24-30; 36pp; Japanese.
XX
XX This invention describes novel anti-NAIP monoclonal antibodies, produced
CC by hybridomas, prepared by fusing antibody-producing cells of mammals
CC immunized with an immunogen containing residues 256-586 or 841-1052 of a
CC 1403 residue amino acid sequence, fully defined in the specification, or
CC their partial sequence, with a myeloma cell line. The monoclonal
CC antibodies are for the study of apoptosis disease onset mechanism,
CC disease diagnosis and development of drugs to prevent and treat
CC apoptosis-related diseases. The quantitation method with the monoclonal
CC antibodies is simple and accurate by using a biological specimen. This
CC sequence represents the human apoptosis inhibitory protein NAIP which is
CC described in the method of the invention.
XX
XX Sequence 1403 AA:

Query Match 100.0%; Score 7308; DB 21; Length 1403;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATQOKASDERISQFDHNLPELSALLGLDAVQALAKELEEBOKERAKMKQKYNQMSRSE 60
Db 1 matqkaaderisqfdhnlpelsaallglдавqalakeleeeqkerakmkqynqmsrse 60
QY 61 AKRLKFTYEPYESSWIMOEMAAAGFYFTGVSKSGTCCCSILRGAGLTRIPIDHKRF 120
Db 61 akrkfttyepyswimqemaagfytgvsksgtccsillrgagltrripiedhkrf 120
QY 121 HPDGFLLNKDVGNIKAKTDIRVKNLKSRLRGKMRQEEEARLASFRRMPFVQGISPCV 180
Db 121 hpdgfllnkdvgniaktdirvknlsrlrgkmrqeeearlasfrmpfvygispvcv 180
QY 181 LSEAGFVFTGKQDVTQVCFSCGCGCLGNWEGDDPMKEHAKMFKCEFLRSKKSSEETQYI 240
Db 181 lseagfvftgkdvtvcfscgcgclgnweegddpmkehakwfkceflrskkseeltqyl 240
QY 241 OSYKFFVDTGHEFVNSVQRELPMASAYCNDISFAYEELRLDSKRDMPRESAVGAAALA 300
Db 241 qsykffvdtghefvnsvqrelpmasaycndisfayeelrlidsrkdmpresavgvaala 300
QY 301 KAGLFYTGKIDVVOGFCGCGCLEKMOEGDDPLDHTRCPPNCPFLONKSSAEVTPDIQS 360
Db 301 kaglfytgkldvvofcgcgclekmoegddpldhtrcppncpflqnmksaeavpdiqs 360
QY 361 RGLCELLETTSESNLIEDSLAVGPIVPEMAOGEAQMFOEAKNINQOLRAAYTSASFRRHMS 420
Db 361 rglcelleettsesnliesdlaavgpivpemaogeaqmfogaeknlneqlraaytsasfrhms 420
QY 421 LLDISSDLATOHLLGCDLSIASKHSKPVQERVLVPEVFGNUNSWCVGEGSGKTIVLL 480
Db 421 lldissdlatohllgcdlsiaskhskpqervlvpevfgnlnswcvcegeasgktivll 480
QY 481 KKIATMASGCCPLNRRPOLVYLLSSTRPEGLASTIICDOLLEKESGVTCMKRNIIO 540
Db 481 kkiatmasgccplnrrpolvyllsstrpeglastiiicdolleksgvctcmkrniio 540
QY 541 QLNKNVLELDDYKEICSGIPQYIGKLIQKNHLSRTCLLAVETNRARDIRAYLETILEIK 600
Db 541 qlknvlelddykeicsgipqyigkqliqknhlsrtcllavetnrrardirayletileik 600

Db 541 qlknqvlflddykeicsipqyigkqliqknhlsrtclllavrtmrardiryletileik 600
QY 601 APPFYNTCIIILAKLFSNHNTRLRKFMVYFGKQKQSIQKIQKTPFLPAALICAHMFQIPEDPS 660
Db 601 appfyntciiiilaklfsnhntrlrkfmvyfgkqkqsiqkiktpflpaalicaahmfqypeds 660
QY 661 PDDVAVFKSVMERLSLRNKATAEILKATVSSCGEALKGFFSCCFEPNDDDLAEGVDED 720
Db 661 pddvavfksvmerslsrnkataeilkatvsscgelalkgffscfepndddlaegvded 720
QY 721 EDLTMCLMSKFTAQRLRPYRFLSPAQOEFILAGMLRELLDSRQEHODLGLYHLKQINS 780
Db 721 edltmclmskftaqrlrpyrflspaqoefilagmlrelldsrqehodlgllyhlkqins 780
QY 781 PMMTVSATYNNFLNYSVSPSTKAGIKYSHLHLVDNKESELENISENDYLLKHQEISIQ 840
Db 781 pmmtvsatynnflnysvspstkagikyshlhlvdkeselenisendylkhqeisiq 840
QY 841 MQLRGIMQICPOAFFSWSEHLVLAKTAVQSNVAAACSPFVLOFQRTLTGALNL 900
Db 841 mqlrgimqicpofswsehlvlatktavqsnvaaacspfvlofqrtrtgaln 900
QY 901 QYFDPHPESLSLRSIHPIRGNKTSPPRAHFSVLETCEDKSGQVPIIDDYASAFEPNEM 960
Db 901 qyfdphpeslslrsihpirgnktspprahfsvleetcgdksgqvpiiddyasafepnem 960
QY 961 EBNLAEKEDNVKSYMDQRRASPDLSGTGWKLSPPQYKIPCELVNDVIDVYGDMLETL 1020
Db 961 ebnlaekednvksymdqrraspsdlsgtgwklspqykipclevndvidvygdmlelt 1020
QY 1021 MTVFASORIEELHNLHNSRFEISIRPALBELSKASYTKCSISKLELSAAQOELLTLPSLE 1080
Db 1021 mtvfasorieelhnlhnsrfeisirpalbelksasytkcsisklelsaagelltlpsle 1080
QY 1081 SLEVSGFTIQSGQDIFPNLDKFLCLAEKLSVLDGNNINVSVPIDEEFPNHMKLLIQISA 1140
Db 1081 slevsgftiqsgqdifpnldkflclaeeklsvldgngninvsvpidfepnhmklliqisa 1140
QY 1141 EYDPSKIVKLIONSPLNHLVFNHLCNPFSDPSGLMTVMVSCKRLTEIKSDSFOAVPFA 1200
Db 1141 eydpskivklionsplnhlvfnhlcnpfsgdpsglmtvmvscrkrlteiksdsoavpfa 1200
QY 1201 SLPNFIKILNLDECOFPDEETSEKFAVILCSLSNLEELIIPTDGIYRVAKLLIQOCC 1260
Db 1201 slpnfikilnldecofpdeetsekfayilcslsnleeliiptdgiyrvaklliqocq 1260
QY 1261 QHCLRLVLSFFKTLNDDSVYELAKVAISGFGQKLENLKSINHKITTEEGYRNFQALDNM 1320
Db 1261 qhclrlvlsffktnddsvyelakvaisgfgklenlksinhkitteegyrnfqaldnm 1320
QY 1321 PMLOELDISRHTTECIKAOATTVKLSQCVLPLRLIRLNLMSWLLDADILLVYMKER 1380
Db 1321 pmlodelisrhtteciakaotvksqcvlplrlirlnlmswlldadillvymker 1380
QY 1381 HPOSKYVLTQIKMILPFSPIIQK 1403
Db 1381 hpqskyvltliqkmilpfspiiqk 1403

RESULT 5
AAW20033
ID AAW20033 standard; Protein: 1403 AA.
XX
XX AAW20033;
XX
XX 06-OCT-1997 (first entry)
XX
XX Neuronal apoptosis inhibitor protein (NAIP).
XX
XX Neuronal apoptosis inhibitor protein; NAIP; diagnosis;
XX therapy; cancer; AIDS; amyotrophic lateral sclerosis;
XX spinal muscular atrophy.
XX

OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Misc-difference 600
 FT /note= "encoded by AAA"
 FT Misc-difference 919 /note= "encoded by CCA"
 FT /note= "encoded by CCA"
 PN M0926331-A2.
 XX
 XX 24-JUL-1997.
 XX
 XX 17-JAN-1997: 97WO-IB00142.
 XX
 XX 19-JAN-1996: 96GB-0001108.
 XX
 PA (UNOT-) UNIV OTTAWA.
 PI Kornejuk RG, Mackenzie AE, Robertson G, Roy N, Tamai K;
 DR WPI: 1997-385335/35.
 DR N-PSDB: AAT71266.
 XX
 PT New neuronal inhibitor of apoptosis - useful for diagnosing and
 XX treating, e.g. cancer, AIDS or amyotrophic lateral sclerosis
 XX
 PS Clatm 41; Fig 7A-L; 102pp; English.
 CC Novel human neuronal apoptosis inhibitor protein (AAM20033), or NAIP,
 CC is a negative regulator of apoptosis, partic. neuronal apoptosis
 CC and, when deficient or absent, contributes to neurodegenerative
 CC phenotypes such as spinal muscular atrophy (SMA) and amyotrophic
 CC lateral sclerosis. Its amino acid sequence was deduced from a
 CC cDNA clone (AAT71266) obtd. from a human foetal spinal cord cDNA
 CC library. NAIP polypeptides, esp. those containing at least two
 CC BIR (baculovirus IAP repeat) domains, can be expressed in host-
 CC vector systems and used to increase or induce apoptosis for the
 CC treatment of AIDS, neurodegenerative disease, myelodysplastic
 CC syndromes or ischaemic injury, to screen for (anti-)agonists, or to
 CC produce antibodies useful for inhibiting apoptosis.
 XX
 XX Sequence 1403 AA:
 SO

Query Match 99.78; Score 7284; DB 18; Length 1403;
 Best Local Similarity 99.78; Pred. No. 0;
 Matches 1399; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

1 MATQOKASDERISQFDHNLPELSALLGLPAYOLAKELREERKERAKKQKGNQSMRSE 60
 1 matqokasderisqfchnlpeelsallglidavlakeleeeekeraakmqkynsqmrse 60
 61 AKRLKTFVTEBPYSSWIPQMAAGFYFTGVKSGICFCSCSLIFGAGLTRLPTEDHKRF 120
 61 akrkltfvtetpyswipqmaagfyftgvksigcfcscslifgagltrlpiedhkrf 120
 61 akrkltfvtetpyswipqmaagfyftgvksigcfcscslifgagltrlpiedhkrf 120
 121 HPDGGFLNKNQGNIAKYDIRVKNLSRLRGCKMRQGEERLASFRNPFYVQGISFCV 180
 121 hpdggflnknqgniakydirvknlsrlrgckmrqgeerlasfrnpfyvqgisfcv 180
 121 hpdggflnknqgniakydirvknlsrlrgckmrqgeerlasfrnpfyvqgisfcv 180
 121 hpdggflnknqgniakydirvknlsrlrgckmrqgeerlasfrnpfyvqgisfcv 180
 181 LSPAGCVFTGKQDTPVCCFCGCGCLGWEEGDDPMKBNKWPFCFPLSKSSSEETIYI 240
 181 lspagcvftgkqdtpvccfcgcgclgweeegddpmkbnkwpfcfplskssseetiyl 240
 181 lspagcvftgkqdtpvccfcgcgclgweeegddpmkbnkwpfcfplskssseetiyl 240
 241 OSYKGFVDITGHEFVSNVQRELPMASAVCNDISFAYEELRLDSKDDPFRSAVGAALA 300
 241 osykgfvdtghefvsnvqrelpmasavcndisfayeelrldskddpfrsavgaala 300
 241 osykgfvdtghefvsnvqrelpmasavcndisfayeelrldskddpfrsavgaala 300
 301 KAGLEPTGKTDLVQCFSCGCGCLEKKWQEGDDPLDHTRCFPCPLQNNKSSAEVTPLOS 360
 301 kagleptgktdlvqcfscgcgclekkwqegddpldhtrcfpcplqnnkssaevtplos 360
 301 kagleptgktdlvqcfscgcgclekkwqegddpldhtrcfpcplqnnkssaevtplos 360
 361 RCELCLELLETSESNTLEDISIAVGPVPEMAGCEAQMFOEAKNLNEOLRAATYSASFRHMS 420

361 rgeclcelletsesnledisavgpvpemaggeaqwfgcaaknleqlraaytsasfrhms 420
 421 LLDISSDILATBHLJCCDLSIASKHISKPOEPLVLEFGNMLNSVMCEGAGSGKTULL 480
 421 lldissdilatbhljccdlsiaskhiskpoeplvlefgnmlnsvmcegagsgktull 480
 421 lldissdilatbhljccdlsiaskhiskpoeplvlefgnmlnsvmcegagsgktull 480
 481 KKAFLMASGCCPLNLRFOLEFVLSLSTRPDEBLASICDQLEKGSVTENCMRNIIQ 540
 481 kkaflmasgccplnlrfolefvlslstprdeblasicdqlekgsvtencmrniiq 540
 481 kkaflmasgccplnlrfolefvlslstprdeblasicdqlekgsvtencmrniiq 540
 541 OLKNQVFLDDYKEIGSIPQVIGTLQKNHLSPTCLLIVAFNRNARDIRRYETLEIK 600
 541 olknqvflddykeigsipqvigtqknhlsptcllivafnrnardirryetleik 600
 541 olknqvflddykeigsipqvigtqknhlsptcllivafnrnardirryetleik 600
 601 AFPEYNTVCLIRKLESHNMRKRFMYFECKNOSLOKIQKTPLEVAICAHMFYFPDS 660
 601 afpeyntvclirkleshnmrkrfmyfecknoslokiktplevaicahmfyfpds 660
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 661 fddvavfksymerlslnkataeilkatvssgcelakgfcscfpfnddlaegvded 720
 661 fddvavfksymerlslnkataeilkatvssgcelakgfcscfpfnddlaegvded 720
 721 EDLTMCMSKFTQORLPRPFRFLSPAFQEFLAGMRLIELDSDROHODLGLYHLKOINS 780
 721 edltmcmskftqorlprpfrflspafqeflagmrlieldsdrohodlgllyhlkins 780
 721 edltmcmskftqorlprpfrflspafqeflagmrlieldsdrohodlgllyhlkins 780
 781 PMKVSAYNNFLNYSVSLPSTRKAPKIVSHLHLVDNKSLEINENDYLRKHOPEISIQ 840
 781 pmkvsaynnflnysvslpstrkapkivshlhlvdnksleinenndylrkhopeisiq 840
 781 pmkvsaynnflnysvslpstrkapkivshlhlvdnksleinenndylrkhopeisiq 840
 841 MQLRLMIOICQAVYSWSEHLLVLAALKTVAVQSNVAACSPFVLQGTETLTGALNL 900
 841 mqlrlmioicqavyswsehllvlaalktvavqsnvaacspfvlqgtetltgalnl 900
 841 mqlrlmioicqavyswsehllvlaalktvavqsnvaacspfvlqgtetltgalnl 900
 901 QTFPHDESLSLRSHIPRIRGNKTSPPRAHPSVLETCDSQOVPIODDYASAEPPNEM 960
 901 qtfphdeslslrshiprirgnktspprahpsvletcdsqovpioddyasaepnem 960
 901 qtfphdeslslrshiprirgnktspprahpsvletcdsqovpioddyasaepnem 960
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 961 ernlaekednvksymdnrbraspdlsitgklskqvikipeclevdvndivvqgdmltel 1020
 961 ernlaekednvksymdnrbraspdlsitgklskqvikipeclevdvndivvqgdmltel 1020
 1021 MTFVSASORIELHUNHSGFTESIRPALELSKASVTGCSITKLELSAEBELITLPSLE 1080
 1021 mtfvasorielhunhsgftesirpalelskasvtgcsitklelsaebelitlpsle 1080
 1021 mtfvasorielhunhsgftesirpalelskasvtgcsitklelsaebelitlpsle 1080
 1081 SLEVSCTGOSQDOIFPNLDRFLCKLELSVDLEGNINVSVIPPEFPFHHMEKTLIQISA 1140
 1081 slevsctgosqdoifpnldrflcklelsvdlengninvsvippefpfhhmektlqiqisa 1140
 1081 slevsctgosqdoifpnldrflcklelsvdlengninvsvippefpfhhmektlqiqisa 1140
 1141 EYDPSKLVKLIONSPLNHLNHFHLKCNFSDGSLMTMYSCKKLTETKFSDFQOAVPVA 1200
 1141 eydpsklvklionsplnhlhnfhhlkcnfsgslmtmysckkltetkfsdfqoavpva 1200
 1141 eydpsklvklionsplnhlhnfhhlkcnfsgslmtmysckkltetkfsdfqoavpva 1200
 1201 SLPEFISLKLINLEGOQFPDEETSEKPAVILGSLMJEELIPTGDIIRVAKLIIQOQ 1260
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 1201 slpefislklinlegoqfpdeetsekpavilgslmjeeliptgdiirvakliiqoq 1260
 1261 QHCLRLVSFFKTLNDSVVEIKVAISGGFOKLEMLKSTINHKITTEBGRNFQALDNN 1320
 1261 qhclrlvsffktlndsveikvaisggfoklemlkstinhkittebgrnfqaldnn 1320
 1261 qhclrlvsffktlndsveikvaisggfoklemlkstinhkittebgrnfqaldnn 1320
 1321 PNLOELISRHFECTKKAQATTVKSLISQCVLRPLIRLMLSWLDDADLALNVNMR 1380
 1321 pnloelISRHFECTKKAQATTVKSLISQCVLRPLIRLMLSWLDDADLALNVNMR 1380
 1321 pnloelISRHFECTKKAQATTVKSLISQCVLRPLIRLMLSWLDDADLALNVNMR 1380
 1381 HPOSKYLTILQKWIIPFPIIOK 1403
 1381 hposkyltilqkwilpfpiioK 1403
 1381 hposkyltilqkwilpfpiioK 1403

RESULT 6

XX Human; apoptosis inhibitory protein; apoptotic disease; diagnosis;
 KW spinal muscular atrophy.
 XX Homo sapiens.
 OS JP1111659-A.
 PN 27-APR-1999.
 PD 14-OCT-1997; 97JP-0280831.
 PF 14-OCT-1997; 97JP-0280831.
 PR 14-OCT-1997; 97JP-0280831.
 XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 PA WPI: 1999-323531/27.
 DR N-PSDB; AAX56273.
 XX New apoptosis inhibitory protein - useful for determining mechanism
 PT of various apoptotic diseases e.g. human spinal muscular atrophy
 PS Claim 1: Page 8-11; 16pp; Japanese.
 CC The present sequence represents a human apoptosis inhibitory protein.
 CC The mechanism of various apoptotic diseases such as human spinal
 CC muscular atrophy and the diagnosis, the prevention and the treatment
 CC of such diseases.
 XX
 SO Sequence 1295 AA;
 Query Match 91.6%; Score 6691; DB 20; Length 1295;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1282; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 OY 1 MATOOKASPERISOPDHNILPELSALIGLDAVOLAKLEEEBOKRAKMOGYNSQMRSE 60
 DB 1 mdtqkadeerdsqtdhnlpeleallgldavqlakeleeceqerkmkgymsqmrse 60
 OY 61 AKRLKFTVTEPYESSWIRPQEMAAGFEYFGVSGISIOCFCCSLIFGAGLTRLPEDHKRF 120
 DB 61 akrktftvtepyeswlrpemaagfyfctgyksqgctccsliffagltrlpiedhkrf 120
 OY 121 HPDGGFLNKKOVNIKAYDITRVKMLKSLRGCKMRVQEEBARLASFRNPFYVOGISPCV 180
 DB 121 hpdggflnkkovnikayditrvkmlksrlgckmrvoeebarlasfrnppyvogispcv 180
 OY 181 LSEAGFVFTGKODTVQCFSCGCGCIGNWEEGDDPMKEHAKMFPKCEPLRSKKSSEITQYT 240
 DB 181 lseagfvftgkodtvqcfscgcgcgignweegddpmkehakmfpkceplrskksseitqyt 240
 OY 241 QSYKGFVDITGEHFNVMWVQRELPMASATCNSDIFAYEELRLDSFKDMPRESAVGVALA 300
 DB 241 qsykgfvditgehfvmwvqrelpmasatcnsdifayeelrldsfkdmprresavgvala 300
 OY 301 KACLFRTTGKIDIVQCFSCGCGCIEKNQEGDDPDDHTRCPPNCPFLQNNKSSAEVTPDLOS 360
 DB 301 kaglftrtgkidiwqcfscgcgcieknqegddpddhtrcppncpflqnnkssaevtpldls 360
 OY 361 RGELCELTETSESNEEDSIANGPIVPEMAQGEAQMFOEAKNLNEQLAATSAFRHMS 420
 DB 361 rgelceltetseesneedsiangpivpemaqgeaqmfoeaknlneqlaatfsafrhms 420
 OY 421 LLDISSDLATDHLGCCDISIAKSHISKPVQEPVLPYFVGUNLNVMCVEGEGSGKTVL 480
 DB 421 lldissdlatdhlgccdisiaskshiskpvqepvlpfyfvgunlnvmcvegegsgktvl 480
 OY 481 KRIATLMAAGCCPLNLRQQLVYLSLSTRPDEGLASICDQLERKSGVTEKMCNIIQ 540
 DB 481 kriaatlmaagccplnlfqvlvylslstrpdeglaslicdqlerksvtekmcniiq 540

OY 541 OLKNDVFLFLDDYKFCISIPQYIGKTIQKNHLSRTCLLIIVRTNRADIRRYETLEIK 600
 DB 541 qlknqvlfllddykfcisipqyigktnhlsrtclliavtrnradirryetleik 600
 OY 601 AFPEFYNTCIIARLFSHNMTLRKRFMYVFGKNOSLOKIOKTPVAAICAHNFQYPPDS 660
 DB 601 afpefyntciiarlfsnmtlrkrfmyvfgknoslokioktpvaaicahnfyppds 660
 OY 661 FDDVAVFKSYMRLSLRNKATAEILKKNVSSCGSLAKGFFSCCFEFDNDLAEACVDD 720
 DB 661 fddvavfksymrlslrnkataelkknvsscgslakgffsccfefnddlaeacvdd 720
 OY 721 EDLTGCLMSKFTTAORLAPFRFLSPAFQEFLLACMRLELSDSDROHODLGLYHLKQMS 780
 DB 721 edltgclmskfttaorlapfrflspafqefllacmrlelstdsdrohodlgllyhlkqms 780
 OY 781 PMMTVSAYNNFLVNVSSLPSTKAGPKIVSHLHLVONKSELENISNDYLRHOPESLQ 840
 DB 781 pmmtvsaynnflvnvsslpstkagpkivshlhlvvnkseleenisndylrhopeslq 840
 OY 841 MOLLRGLOICPOAFSVMSEHLVLALKTAVQSMNTVAACSPFVLQFLOGRTLTGALNL 900
 DB 841 mqlrlglwqlcpqayfsmvsehlvlalktavqsmntvaacspfvqlfgtrtltgaln 900
 OY 901 QYFDPHESLTLRSIHPIRGNKTSPPRAHFSVLETCEDKSGVPTIODOVASAFPMNW 960
 DB 901 qyfdphesltslrshpigrnktspprahfsvleetcidksqvptiodovasafpmnw 960
 OY 961 ERNLAKEDNVKSYMOMKORASPDLSYGWKLSPKQYKIPCLLEVANDIDVQGMLEIL 1020
 DB 961 ernleakednvksymomkoraspdlsygwklspkqykiplevandidvqgdmleil 1020
 OY 1021 MIVFSAQSRIELHLNHSRGFIESIRPALELSKASVTCOSISKLSAABOELLTPSLE 1080
 DB 1021 mivfqsasqriehlhnhsrgfiesirpalelskasvtcosisklsaaobeltpsl 1080
 OY 1081 SLEVSGTIOSDOLFPNNDKFLCLKEISVDLEGINVFSVPIEFPMHNEKTLQISA 1140
 DB 1081 slevsgtiosdolfpnnkflclkeisvdeginvsvpiefpmhnektlqisa 1140
 OY 1141 EYDSKLVKLLQNSPMLHVFHLCNFSDFGSLMTMLVSCCKTLEIKFSDFQAVPVA 1200
 DB 1141 eydsklvkllqnspmhvfhlcnfsgfslmtmlvsccktleikfsdfqavpva 1200
 OY 1201 SLNPFISLKLINLEGOFPDEETSEKRAYILGSLSLBELLPFGDIYRVAKLIQOCQ 1260
 DB 1201 slnplfisklinlegofpdeetsekrayilgslslbellpfgdiyrvakliiqocq 1260
 OY 1261 OLHCLRLSFFKTLNDSVVEIAKV 1285
 DB 1261 olhclrlsffktnldsvveigel 1285
 RESULT 8
 AAR98217
 ID AAR98217 standard; Protein; 1232 AA.
 XX
 AC AAR98217;
 XX
 DT 30-DEC-1996 (first entry)
 XX
 DE Neuronal apoptosis inhibiting protein.
 XX
 KW Neuronal apoptosis inhibiting protein; human; NAIP; chromosome 5q13; VAC;
 KW yeast artificial chromosome; spinal muscular atrophy; mammalian cell;
 KW autosomal recessive; neurodegenerative disorder; alpha motor neuron; SMA;
 XX spinal cord; proximal voluntary muscle; therapy; apoptotic mechanism.
 OS Homo sapiens.
 XX
 PN W09612016-A1.
 XX
 PD 25-APR-1996.

XX 17-OCT-1995: 95MO-CA00581.
 XX
 PF 19-DEC-1994: 94CA-2138425.
 PR 18-OCT-1994: 94GB-0021019.
 XX
 PA (SHKJ) RES DEV CORP JAPAN.
 XX (UYOT-) UNIV OTTAWA.
 PI Ikeda J, Korneluk RG, Mackenzie AE, Mahadevan MS;
 PI Mclean M, Roy N;
 XX WPI: 1996-222003/22.
 DR N-PSDB: AAT30092.
 XX
 PT Neuronal apoptosis inhibitor protein gene - used to develop prods.
 PT for use in the diagnosis and therapy of spinal muscular atrophy
 XX
 PS Claim 3; Page 68-70; 113pp; English.
 XX
 CC This sequence represents the human neuronal apoptosis inhibitor protein
 CC (NAIP). The cDNA encoding this sequence was found on a region of the
 CC human chromosome 5q13. This sequence was isolated from a yeast
 CC artificial chromosome (YAC) contig containing the D5S435-D5S112 interval
 CC of the chromosome 5q13. Mutations in the NAIP gene, are causative of
 CC spinal muscular atrophy (SMA) types I, II, and III. SMAs are a group of
 CC autosomal recessive, neurodegenerative disorders. SMAs are classified
 CC into the three types based upon the age of onset (with type I being the
 CC severest form with the earliest age of onset). All three types are
 CC characterised by the degeneration of the alpha motor neurons of the
 CC spinal cord manifesting as weakness and wasting of the proximal voluntary
 CC muscles. The most common mutations of the NAIP gene sequence are thought
 CC to be deletions of exons 5 and 6, and reductions in the copy number of
 CC the gene. The NAIP gene, (and primers and probes based on it) can be
 CC used for the diagnosis of SMA, and for directing the formulation of
 CC conventional and genetic therapies for SMA. Identification of genes
 CC showing homology with the NAIP locus, and proteins that interact with
 CC NAIP can be used in the elucidation of apoptotic mechanisms in mammalian
 CC cells.
 CC
 XX
 XX Sequence 1232 AA:
 SO

Query Match 87.2%; Score 6373.5; DB 17; Length 1232;
 Best Local Similarity 95.9%; Pred. No. 0;
 Matches 1222; Conservative 1; Mismatches 1; Indels 51; Gaps 1;

Db 361 rgelcelltetsesnledsiavgpiivpemaqgeaqvfgkdnloeqlraeytsasfrms 420
 QY LLDISSDIAATHLGGCDLSINASKHSKRVQEPVLPVFGMLNNSWMCYEGSAGSKTYLL 480
 Db 421 LLDISSDIAATHLGGCDLSINASKHSKRVQEPVLPVFGMLNNSWMCYEGSAGSKTYLL 480
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 QY KRIAFIAGSGCCPLNRFQALVFLSYLSSTRPDEGLASIIICQOLEKEGSVTEMCARNIIQ 540
 Db 481 KRIAFIAGSGCCPLNRFQALVFLSYLSSTRPDEGLASIIICQOLEKEGSVTEMCARNIIQ 540
 Db 481 KRIAFIAGSGCCPLNRFQALVFLSYLSSTRPDEGLASIIICQOLEKEGSVTEMCARNIIQ 540
 QY QLNQOVFLDDYKEIGSIPQVIGKLIQKNHLSRTCLLIAVTRNARDIRRYLETIEIK 600
 Db 541 QLNQOVFLDDYKEIGSIPQVIGKLIQKNHLSRTCLLIAVTRNARDIRRYLETIEIK 600
 QY qkngvlflddykeicsipqvigklqknhlstrclliavtrnarrdrryletieleiq 600
 Db 541 qkngvlflddykeicsipqvigklqknhlstrclliavtrnarrdrryletieleiq 600
 QY AAPPFNVCILIRKLESHMTRLRKRNVEFGNQSLOKOKTPPLFAACAMFOYPPPS 660
 Db 601 AAPPFNVCILIRKLESHMTRLRKRNVEFGNQSLOKOKTPPLFAACAMFOYPPPS 660
 QY afpfnvvcilrklrshmtlrlrkrmvfygknsglqkqkplvvaalcawfgpdpds 660
 Db 601 afpfnvvcilrklrshmtlrlrkrmvfygknsglqkqkplvvaalcawfgpdpds 660
 QY FDDVAVFESYMERLSLRNKATAEILKATVSSCGELATKGFFSCCFEFDNDLAEAGVDED 720
 Db 661 FDDVAVFESYMERLSLRNKATAEILKATVSSCGELATKGFFSCCFEFDNDLAEAGVDED 720
 QY fddvavfesymerlslnrkataeilkatvsscgelatkqffscctefnddlaeagvded 720
 Db 661 fddvavfesymerlslnrkataeilkatvsscgelatkqffscctefnddlaeagvded 720
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 Db 721 EDLFWCLMSKFTPAQRLPFFYFLSPAFOEPLAGMKLELDDSDROHODLGLYHLKQINS 780
 QY edlfwclmskftpaqrlrpfyflspafoeplagmklelldsdreqhqdglglnlkqns 780
 Db 721 edlfwclmskftpaqrlrpfyflspafoeplagmklelldsdreqhqdglglnlkqns 780
 QY PMKTVSATANNLNYVSSLPSTKAGKIVSHLHLVDNKNESLENDSNDYIAKHQPEISIQ 840
 Db 781 PMKTVSATANNLNYVSSLPSTKAGKIVSHLHLVDNKNESLENDSNDYIAKHQPEISIQ 840
 QY pmtvsaaynnllyvsslpstkaqpklvshllhvdnknslensnddyikhpeisliq 840
 Db 781 pmtvsaaynnllyvsslpstkaqpklvshllhvdnknslensnddyikhpeisliq 840
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 Db 841 MOLLRLGLOIQPOAFVSWSEHLVLAUKTAYQSTVAAVSPVYQFLOGRTLTGALNTL 900
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 Db 841 mllrlglqloqpoafvswsehlvlyauktayqstvacaspvlyqflogrtltlgaln 900
 QY QYFDPHPSLSLRSIHPPRGNKTSPPRAHFSVLETCFDKSQVPTIIDDYASAEPPNNEW 960
 Db 901 QYFDPHPSLSLRSIHPPRGNKTSPPRAHFSVLETCFDKSQVPTIIDDYASAEPPNNEW 960
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 Db 901 qyfdhpslsllrsihpprgnktspprahfsvleetcfdksqvpitiddyasafepnnew 960
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 Db 961 ERNLAEREDNYSVWDMQRRASPOLSTGYWKLSPKQYIIPCLEVDVNDIVVGGOMLETL 1020
 QY ernlaekednysvwdmqriraspolstgywklspkqykipclevdvndidvvgqdmlel 1020
 Db 961 ernlaekednysvwdmqriraspolstgywklspkqykipclevdvndidvvgqdmlel 1020
 QY MTFVSASORIELNLNHSRGFTESIRPALETSKASVTKCSIKLELSAAEOLLETLPSLE 1080
 Db 1021 MTFVSASORIELNLNHSRGFTESIRPALETSKASVTKCSIKLELSAAEOLLETLPSLE 1080
 QY mtvfasorielnlhnsrgftesirpaleltskavtkcsiklslsaeqelltlpsle 1080
 Db 1021 mtvfasorielnlhnsrgftesirpaleltskavtkcsiklslsaeqelltlpsle 1080
 QY SLEVSCTIOSQDIFPNLDKFLCLKELSVDLGCNINVSFVPEEPFNHMEKLLIQISA 1140
 Db 1081 SLEVSCTIOSQDIFPNLDKFLCLKELSVDLGCNINVSFVPEEPFNHMEKLLIQISA 1140
 QY slevsctiqsqdipnldkflclkelsvdlgcnnvsvfpeefpnhmeklllqisla 1140
 Db 1081 slevsctiqsqdipnldkflclkelsvdlgcnnvsvfpeefpnhmeklllqisla 1140
 QY EYDPSKLVKLONSPNLAVPHLKCMEFSDGSLMTMLVSCAKLLEIKFSDFSFPQAVPPVA 1200
 Db 1141 EYDPSKLVKLONSPNLAVPHLKCMEFSDGSLMTMLVSCAKLLEIKFSDFSFPQAVPPVA 1200
 QY eydpsklvklonspnlavphlkcme fsdgslmtmlvscaklleikfsdfsfpqavppva 1200
 Db 1141 eydpsklvklonspnlavphlkcme fsdgslmtmlvscaklleikfsdfsfpqavppva 1200
 QY SLNPFISLKLINLEGOFPDEETSEKPAYILGSLNLEELIIPMGDIYRAKLLIQOCC 1260
 Db 1201 SLNPFISLKLINLEGOFPDEETSEKPAYILGSLNLEELIIPMGDIYRAKLLIQOCC 1260
 QY slnplfisklilnleqqpdpdeetsekpayilgslslneelllppgdgylrraklllqqcc 1260
 Db 1201 slnplfisklilnleqqpdpdeetsekpayilgslslneelllppgdgylrraklllqqcc 1260
 QY QLHCLRLVSFEKTLNDSVVEI 1282
 Db 1210 QLHCLRLVSFEKTLNDSVVEI 1282
 QY qlhclrlvsfektlnndsveel 1231
 Db 1210 qlhclrlvsfektlnndsveel 1231

RESULT 9
 AAU02881
 ID AAU02881 standard; Protein: 1204 AA.
 XX
 AC AAU02881:
 XX
 DT 12-SEP-2001 (first entry)
 XX
 XX Human caspase recruitment domain 12 (CARD-12) polypeptide #2.
 DE
 XX

[illegible][illegible]


```
Db      877 vlegltalmipwgcvgsslsllkhlvevpqlvklgnwrltdt-----elrllgaff 931
Oy      1292 -----QKLENKLSTINHKITEGYNRFQALDNMPNLELDISRHFTEGICAKOATTVKSL 1346
Db      932 gknplknfvgqlnlaqn-rvssdgwlaimgvfenlkqlvffdfs---tkeflpdpalvrlk 987
Oy      1347 SOCVLRPLRLRLNMLSMILLDADIAL 1374
Db      988 sqvisklctflgearlvwgqfdddlsvi 1015

RESULT 12
AAM23595
ID      AAM23595 standard; Protein; 841 AA.
XX
AC      AAM23595;
XX
DT      12-OCT-2001 (first entry)
XX
DE      Murine EST encoded protein SEQ ID NO: 1120.
XX
KW      Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW      tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW      diagnostics; forensic test; gene mapping; genetic disorder;
KW      biodiversity; gene therapy; nutrition.
XX
OS      Mus musculus.
XX
PN      WO200154477-A2.
XX
PD      02-AUG-2001.
XX
PF      25-JAN-2001; 2001WO-US02687.
XX
PR      25-JAN-2000; 2000US-0491404.
PR      17-JUL-2000; 2000US-0617746.
PR      03-AUG-2000; 2000US-0631451.
PR      15-SEP-2000; 2000US-0663870.
XX
PA      (HWE-) HYSEQ INC.
XX
PI      Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI      Cao Y, Dermanac RA, Zhang J, Werhman T;
XX
DR      WPI: 2001-476164/51.
DR      N-PSDB: AAH98254.
XX
PT      Isolated polypeptide for treatment of diseases, diagnostics, raising
PT      antibodies and research use -
XX
PS      Claim 20; Page 832-833; 1275pp; English.
XX
CC      The present invention provides the protein and coding sequences of novel
CC      proteins from a variety of organisms, including human, dog, cat, horse,
CC      cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC      urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC      from the organism of interest. They can be used in diagnostics,
CC      forensics, gene mapping, identification of mutations, to assess
CC      biodiversity and for nutritional purposes. The present sequence is a
CC      protein of the invention.
XX
SQ      Sequence      841 AA;

Query Match      7.7%; Score 566; DB 22; Length 841;
Best Local Similarity 23.5%; Pred. No. 3, 1e-38;
Matches 226; Conservative 174; Mismatches 359; Indels 202; Gaps 36;
```

```
Db      60 vllfllldgynef--kpnqnceieallkenhrfkmvvtvtteclrlhrrfgalteevgdm 117
Oy      603 pEYNTVCILRKLEFSNMTLRKRMVYFGKNOSLOKIQKTPLEVAICAMFOYPEPDSFD 662
Db      118 tedsaqallrevllikela--eglllgkscrlnmkcpflvltcalqmgsefshnt 175
Oy      663 DVAVFYSYMERLSLRK-----ATAEIUKATVSSGGEALALGFPSCCFEFDNDLAEG 716
Db      176 qtlfhttydlilqknkhkhkvaadflr-sldhcyalalegvishkldfelydv--ss 232
Oy      717 VDEEDLTWCLMSKFPNQRPLRPFRPLSPAFQEFGLARLELLEDDROEHODGLGYHKK 776
Db      233 vnedvlltctgllckytaqgfkpkkykfhsfgeytagrllslltchepeertkngnylq 292
Oy      777 QINSPMTVSAYNNFLNLY--SLSPSTKAGPIVSHLHLVDN-----KE 819
Db      293 kmvslsdlstysllrycgssveatra---vmkhlaavyqhgcllgistakrplwrqe 349
Oy      820 SLENISENDYLKHQPEISLOQMLRGLMOICQAFVSMSVSEHLVLAKTAYQST-VA 878
Db      350 slqsvkn-----tlegelika1---nlhsfvecgllh-----ygestsks 386
Oy      879 ACSPEVLQFQGRTRLGALNL-QYFDPHPESTLSLSIHPIRGKNTSPRAHFSVLETC 937
Db      387 alsqefaeafgqskslsyngnlpdyldfite-----hlp-----420
Oy      938 FKSQVPTIDODYASAFE-----PNNEWRNLAEKEDNVKSYMDMORRASPDLSTG 988
Db      421 -----ncasaldfikllygygamasve-----Kaeedtgyl 451
Oy      989 YMKLSPKOYKIP-----CLEVYNDIDVYGDMLELMTVFSASQRIELH 1033
Db      452 hmeeaepely-tpsravslffnwqgeftrlevltdtsklnkqdlrylghkfsatslrlq 510
Oy      1034 LNHSGFIESIRPALBELSKASVTKCSISKLELSAAQELTLTPSLESLEVSQTIQSDQ 1093
Db      511 krcagvagslsavlstck-nlslmveaspltdederhltsvtnlktslnh---dlqng 566
Oy      1094 IEPN--LDKFLCLKELSYDLEGNINVSVPPEFPNHHMKLLIOISAEYDPSKLVKLI 1151
Db      567 rlpqgltdslgnlknltkljmdnkm-----needaiklaeg1 604
Oy      1152 QNSPNLHVHFLKCNFSDSGSLMTMLYS-----CKLIREKSDSFF--QAVPFA-SL 1202
Db      605 kolkmclthl--thtsldlgemdylvkslsepc-dleelqivscslsanaaklllaqn1 661
Oy      1203 PNFISSKILNLEGOQFPDETSERFAYILGSLSNLEE---LILPTGDIYRVAKLIIQOC 1259
Db      662 hnlvkslstdl-senylekdgnealhelldrmvleqalcmlpwgcvtqgsislkh1 720
Oy      1260 QQLHCLRVLSFEKTLNDSDVETAKVAISGCF-----QKLENKLSTINHKITEEGYRNF 1313
Db      721 eevpqvklvklgnwrltdt-----elrllgafgknplknfvgqlnlaqn-rvssdgwla1 774
Oy      1314 FOALDNMPNLELDISRHFTEGICAKATYKSSOCVLRPLRLRLNMLSMILLDADIAL 1373
Db      775 mgyfenlkqlvffdfs---tkeflpdpalvrlklsqvisklctflgearlvwgqfdddlsv 831
Oy      1374 L 1374
Db      832 I 832

RESULT 13
AAB53493
ID      AAB53493 standard; Protein; 118 AA.
XX
AC      AAB53493;
XX
DT      09-MAR-2001 (first entry)
XX
DE      Human colon cancer antigen protein sequence SEQ ID NO:1033.
```

XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW Identification: cytostatic; cardiotoxic; neuroprotective; vullnary;
 KW immunomodulatory; muscular; gynaecological; gastrointestinal;
 KW nephrotoxic; antineoplastic; antibacterial; gene therapy; wound;
 KW reproductive disorder; immune system disorder; muscular disorder;
 KW Infectious disease; gastrointestinal disorder; renal disorder;
 OS Homo sapiens.
 PN WO200053531-A1.
 PD 21-SEP-2000.
 PF 08-MAR-2000; 2000MO-US05883.
 PR 12-MAR-1999; 99US-0124270.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Ruben SM;
 DR WPI: 2000-587534/55.
 DR N-PSDB: AAC98250.
 PT Colon cancer associated gene sequences, referred to as colon cancer
 PT antigens, useful for the treatment, prevention, and diagnosis of colon
 PT disorders such as colon cancer -
 XX
 XX Claim 11: Page 1612; 2104pp; English.
 XX
 CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,
 CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
 CC human colon cancer antigens can have cytostatic, cardiotoxic, muscular;
 CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
 CC vullnary, nephrotoxic, antineoplastic, antibacterial, gene therapy, wound;
 CC can be used in gene therapy. The colon cancer antigen polynucleotides,
 CC proteins and antibodies to the proteins are useful for the prevention,
 CC treatment and diagnosis of colon disorders, such as colon cancer. The
 CC polynucleotides may be used in diagnostics and research, such as for
 CC chromosome identification, and as hybridisation probes. The proteins
 CC may also be used to prevent diseases such as neural disorders, immune
 CC system disorders, muscular disorders, reproductive disorders, immune
 CC gastrointestinal disorders, wounds, renal disorders, infectious
 CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
 CC AAB54007 represent sequences used in the exemplification of the present
 CC invention.
 XX
 XX Sequence 118 AA:
 SQ
 Query Match
 Best Local Similarity 7.5%; Score 545.5; DB 21; Length 118;
 Matches 106; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
 QY 607 TGCILRLKLFHNMTRLRKFMVYFGKNSLOKOTPLFPAATCAIMFQYPPDPSPDVAV 666
 DB 1 Tvcilrlkflshnmtrlrkfmvyfgknsiqkqkplfvaaicaiahfydpdpdvdav 60
 QY 667 FKSVMERLSLRNKATAEILKATVSSCGELALGFCFCEFFND-DDLAEG 716
 DB 61 fksymelrlslrnkataelilkatvsscgealalgfcfcfeffngmmdlaeg 111
 RESULT 14
 AAC67526
 ID AAC67526 standard; Protein: 738 AA.
 AC AAC67526;
 XX
 DT 26-NOV-2001 (first entry)
 XX

DE Amino acid sequence of a human secreted polypeptide.
 XX
 KW Human; secreted polypeptide; nervous disease; muscular disease; tumor;
 KW gastrointestinal ulceration; spinal cord disease; trachea disease;
 KW thyroid gland disease; ovary disease; prostate disease; heart disease;
 KW renal gland disease; small intestine disease; thymus disease;
 KW lymph node disease; muscular system disease; colon disease;
 KW lipase deficiency; cystic fibrosis; pancreatitis; clot formation;
 KW myocardial infarction; angioplasty; liver disease; coagulation disorder;
 KW microbial disease; immune disorder; inflammation; transplant rejection;
 KW bone thickness; bone density; ferrooxidase loss; apoptosis;
 KW vascular smooth cell proliferation; vaccine.
 XX
 OS Homo sapiens.
 PN WO200166690-A2.
 PD 13-SEP-2001.
 PF 05-MAR-2001; 2001MO-US07143.
 PR 06-MAR-2000; 2000US-0187107.
 PR 13-MAR-2000; 2000US-0188916.
 PR 03-OCT-2000; 2000US-0236874.
 PR 03-OCT-2000; 2000US-0237846.
 PA (SMK) SMITHKLINE BEECHAM CORP.
 PA (SMK) SMITHKLINE BEECHAM PLC.
 PI Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;
 XX
 XX WPI: 2001-570768/64.
 DR N-PSDB: AAB78218.
 PT Novel isolated secreted polypeptide useful for treating nervous and
 PT muscular diseases, gastrointestinal ulceration, coagulation and immune
 PT disorders, microbial diseases, inflammation and transplant rejection -
 XX
 XX Claim 1: Page 89-91; 102pp; English.
 XX
 CC The present sequence represents a human secreted polypeptide. The
 CC secreted polypeptides and polynucleotides are useful for treating
 CC nervous and muscular diseases, for inhibiting tumor formation and
 CC metastasis, for treating gastrointestinal ulceration, for preventing
 CC and treating diseases in spinal cord, thyroid gland, ovary, prostate,
 CC renal gland, small intestine, heart, trachea, thymus, lymph node,
 CC muscular system and colon, for treating lipase deficiency in cystic
 CC such as myocardial infarction, during angioplasty and all surgical
 CC procedures that require decreased blood clot formation, for treating
 CC liver diseases, coagulation disorders and microbial diseases, for
 CC treating immune disorders, for treating inflammation and transplant
 CC rejection, for enhancing bone thickness and increasing bone density,
 CC apoptosis, and for regulating vascular smooth cell proliferation. They
 CC may also be used as vaccines.
 XX
 XX Sequence 738 AA:
 SQ
 Query Match
 Best Local Similarity 7.3%; Score 536.5; DB 22; Length 738;
 Matches 197; Conservative 142; Mismatches 285; Indels 181; Gaps 29;
 QY 344 FLQNMKS-SAEVTPDLOSREICELLETSSNMEDSIAGVIVPEMAGGEQWQEKKN 402
 DB 55 flkslkemypilfgdngq-----slfhtsegdlld----- 86
 QY 403 LNEOLRAAYTSASFRRHMSLDISSDLATDHLGCOLST---ASKHISPV----- 449
 DB 87 laqdlkdxlthpseflnf-----ypigedidilfnlksfltepyvlwkdqhhnr 134
 QY 450 QEPVLVPEVFGNLSVMCVGEAGSGKTVLLKIAFLWASGCCPLNRPOLVYPLSLST 509

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Db 135 veqllingllqalspcilegesgkgtcllqrlamllwsgskckaltkfkfvtllrls-- 192
Qy 510 RPDEGLASITCDLLEKSGSTEMCRNIIOQLKNQVFLDDYKREISIQ--VIGKL 566
Db 193 ragglllectldcdldlpgtlrktqtfmamlklqrvllldgynef--kqncpeleal 250
Qy 567 IOKNHLSTCLLIIVRTNRARDIRYLETLEIKAFPPYVNCIRKLFSSHMTFLRKFM 626
Db 251 lkenhrfmmivtttctclhlrtqfqltaevgmdtsdqaalirevllkeila--egll 308
Qy 627 VYFGKNSIQRIOKTPLEVAACAHMFQYPPDPSPFDVAVERKSYMERLSLRNK-----A 680
Db 309 lqtkscrlrlmktprlvtlcalqmgeseftshltqcltftfydlllqknkhkhgva 368
Qy 681 TAEILIKATVSSCGELAKGFFSCCFEENDDLAEGVDEDEDLTMCLMSKPTAQLRPFY 740
Db 369 asdftr-sldhcgdlalegvfshktdfelqdv--ssvnedvllltgllckytaqrfkpk 425
Qy 741 RFLSPAFQEPFLAGMRLEILDSRQEHODLGLYHLKQINSPMTVSAVNNFLNYV--SSL 798
Db 426 kfhkstfgeytagrrlslsltshepevckngyldkmvslsdtslysllytcgssv 485
Qy 799 PSTKAGPKIVSHLHLVDN-----KESLENISENDYDLKHQPEISIQMQL 843
Db 486 eatra--vmkhlaevyhgcllglstakrplwrqeslqsvkn-----ttegei 531
Qy 844 LRGLMQICPQAFVSMVSHLVLVLAKTAYQSNF--VAACSPYVLOLQGRITLGLALN--Q 901
Db 532 lka1---nlnstfvecghl-----ygestskalsqfeafelggksilynsqnlpd 579
Qy 902 YFFDHPESLILRSIHPIRGNKTSBRAHFSVLETCFPOKSOVPTIDOOYASAFERPMNE 961
Db 580 ylfid-----flehlpnc--asaifklidfygg--amasve 611
Qy 962 ENLAEKEDNVKSYMOMRASPDLSTGYWKLSPKQKIP-----CLEVDY 1006
Db 612 -----kaeedtgylmneapeyl-lpravslffnwkgqftrlevtl 652
Qy 1007 NDIDVVGDMLEILMTVVSASORIELHLNHSNGFTESIRPALELSKASYTKCSIKLEIS 1066
Db 653 rdfsrlnkqdlrlylqklissatsrlqlkrcagvagslslvstck-nlyslmveaspl 711
Qy 1067 AAODELLTLPLSLEVSIGTIOG 1091
Db 712 lederhltsvtnlkltsln-dlqng 735

RESULT 15
AAW19746
ID AAW19746 standard; Protein: 618 AA.
AC AAW19746;
XX
AC AAW19746;
XX
DT 16-SEP-1997 (first entry)
XX
DE Human inhibitor of apoptosis protein homologue M1HB.
XX
KW Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; M1HB;
KW degenerative disease; infectious disease; autoimmune disease;
KW cancer; therapy; diagnosis.
XX
OS Homo sapiens.
XX
FH Key
FH Location/Qualifiers
FT 46..113
FT /label= BIR
FT 184..250
FT /label= BIR
FT 269..337
FT /label= BIR
FT 569..606
FT /label= RING_finger
FT Region
FT Region

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XX
PN W09723501.A1.
XX
PD 03-JUL-1997.
XX
PF 20-DEC-1996; 96WO-AU00827.
XX
PR 22-DEC-1995; 95AU-0007275.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Vaux DL;
XX
DR WPI: 1997-350966/32.
XX
N-PSDB: AAT72711.
XX
PT Isolated protein homologues of viral inhibitors of apoptosis - used
PT to modulate apoptosis for treatment of degenerative, infectious or
PT autoimmune diseases and cancer
XX
PS Claim 8; Page 51-54; 136pp: English.
XX
CC Mammalian IAP homologue B (M1HB) (AAW19746) is a human homologue of
CC baculovirus inhibitor of apoptosis protein (IAP). Its amino acid
CC sequence was deduced from a cDNA clone (see also AAT72711) isolated
CC from a human foetal liver cDNA library using primers based on
CC human EST sequences that resembled the BIR repeats of Orygia
CC pseudotsuguta polyhedrosis virus IAP. IAP homologues (see also
CC AAW19745 and AAW19747-52) and their derivatives and chemical analogues
CC can be used in methods for modulating apoptosis in animal cells,
CC specifically for treatment, by inhibition, of degenerative and
CC infectious disease or, by promotion, of cancer and autoimmune
CC disease.
XX
SQ Sequence 618 AA:

Query Match 6.3%; Score 462; DB 18; Length 618;
Best Local Similarity 26.0%; Pred. No. 1,Je-29;
Matches 155; Conservative 82; Mismatches 214; Indels 146; Gaps 22:

Qy 38 LEEEDOKERAKQKQYNSQMRSEARKLRTFYEPYSSWIP---QEMAAAGFYPTGVKSG 94
Db 28 lsdwcnshkqkmkydfsee-----lymstysftfpgypvsestlraglygyvndx 80
Qy 95 IQCFCCSLILFGAGLRLPIEDHKRFRHPDCGF---LANKDGNIAKYDIRVKN----- 144
Db 81 vkfcfcgimldmwlqgdsplqkqlypscfifqnlvsalsgstskntspmrnsfahals 140
Qy 145 -----LKSRL-----RGCKMY--QEEFARLASFFNNPFYVG 175
Db 141 ptlehsllfsgysalspnlinsravedlssrtlpysamteearcltlymwp--llf 198
Qy 176 ISPCVISEAGFYFTGKODTVOCFSCGCGICGANEEDGDPKREHAKWPKCEFRSKSSEE 235
Db 199 lspselaragfyyigpdtvacfaagkylswepkddamseirtrfncpfl-----ensle 255
Qy 236 ITQYIQSYKGFVDITGEHFVNSWVRELPMASAYCNDISIFAYEELRLDSFKDMPRESAVG 295
Db 256 tlrfsls-----nlsmqt-----haartmftlmwpsvvpq 286
Qy 296 VAALKAGLFTYGINDIYOCFSCGGLKFMQSGDDPLDDHTRCFPNCPLQNMKSSAEVT 355
Db 287 peglasagfyyvgrndvkcctcdgglctwesgddpwehkwfprceflilmkqg-efv 345
Qy 356 PDLOQR-GEIACEILETTSESINLEDSIAVGPIYPEMAOGSEAWFOEAKMLNEOLRAAYTSA 414
Db 346 deiggrtyphllleqllstsdtegen--adpplihgpgess--sedavmmntprvvsaleem 402
Qy 415 SFRHMSLDDISSDLATDHLILGCDLSIAKHKISKPVQEP-LVLPVFGNLNMYCYEGEAG 473
Db 403 gfnr-----dl-----vkqvgsklilttgenyktvndivsalinae 438

```

OY 474 SGTVLK-KIAFLWASGCCPLNRFOLVFLSLSTRPDEGLASICDQLEKEGSYTE 532
Db 439 dekseekekqaeasddlsllrkrmalfgqlcvlp-----lIdnllk----- 484
OY 533 MCMRNIOQLKQVLFLLDVKKEICSPOVIGKLIQKNHLSRTCLLAVRTNRARDI 589
Db 485 ---anvlnkqehdl-----kqktqplqarelId-----tlivkgnaaanl 523

Search completed: September 30, 2002, 15:04:43
Job time: 324 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 30, 2002, 15:00:54 : Search time 19.98 Seconds
(without alignments)
1715.171 Million cell updates/sec

Title: US-09-830-338-1
Perfect score: 7308
Sequence: 1 MATOQKASDERISQFDHNL.....SKYTLILQKWLPSPILQK 1403

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued_Patents_AA:*
2: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6373.5	87.2	1232	3	US-08-836-134-2
2	5955	81.5	1151	3	US-08-836-134-23
3	462	6.3	618	2	US-08-511-485-8
4	462	6.3	618	3	US-09-212-971-8
5	462	6.3	618	4	US-08-800-929A-8
6	462	6.3	618	4	US-08-569-749-2
7	462	6.3	618	4	US-09-617-053A-8
8	462	6.3	618	4	US-09-069-023-29
9	462	6.3	618	5	PCT-US96-12860-2
10	457.5	6.3	612	4	US-09-212-971-14
11	457.5	6.3	612	4	US-08-800-929A-14
12	457.5	6.3	612	4	US-08-569-749-14
13	457.5	6.3	612	4	US-09-617-053A-14
14	457.5	6.3	612	5	PCT-US96-12860-14
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16	440	6.0	600	4	US-08-800-929A-12
17	440	6.0	600	4	US-09-617-053A-12
18	437.5	6.0	496	2	US-08-511-485-10
19	437.5	6.0	496	3	US-09-212-971-10
20	437.5	6.0	496	4	US-08-800-929A-10
21	437.5	6.0	496	4	US-09-617-053A-10
22	436.5	6.0	604	4	US-08-569-749-4
23	436.5	6.0	604	5	PCT-US96-12860-4
24	431.5	5.9	604	2	US-08-511-485-6
25	431.5	5.9	604	3	US-09-212-971-6
26	431.5	5.9	604	4	US-08-800-929A-6
27	431.5	5.9	604	4	US-09-617-053A-6

28	403	5.5	497	2	US-08-511-485-4	Sequence 4, Appl1
29	403	5.5	497	3	US-09-212-971-4	Sequence 4, Appl1
30	403	5.5	497	4	US-08-800-929A-4	Sequence 4, Appl1
31	403	5.5	497	4	US-09-617-053A-4	Sequence 4, Appl1
32	340.5	4.7	438	5	PCT-US95-05922A-2	Sequence 2, Appl1
33	337	4.6	498	2	US-08-511-485-13	Sequence 13, Appl1
34	303.5	4.2	275	2	US-08-511-485-12	Sequence 12, Appl1
35	303.5	4.2	275	3	US-08-836-134-21	Sequence 21, Appl1
36	293.5	4.0	268	3	US-08-836-134-22	Sequence 22, Appl1
37	290	4.0	50	4	US-08-975-080-26	Sequence 26, Appl1
38	261	3.6	47	4	US-08-975-080-13	Sequence 13, Appl1
39	212.5	2.9	68	2	US-08-511-485-27	Sequence 27, Appl1
40	209.5	2.9	236	4	US-09-121-979-4	Sequence 4, Appl1
41	209.5	2.9	236	4	US-09-332-319-4	Sequence 4, Appl1
42	207.5	2.8	68	2	US-08-511-485-26	Sequence 26, Appl1
43	200.5	2.7	68	2	US-08-511-485-20	Sequence 20, Appl1
44	196.5	2.7	68	2	US-08-511-485-21	Sequence 21, Appl1
45	185.5	2.5	68	2	US-08-511-485-28	Sequence 28, Appl1

ALIGNMENTS

```
RESULT 1
US-08-836-134-2
: Sequence 2, Application US/08836134A
: Patent No. 6020127
: GENERAL INFORMATION:
: APPLICANT: Mackenzie, Alex E.
: APPLICANT: Korneluk, Robert G.
: APPLICANT: Mahadevan, Mani S.
: APPLICANT: Mclean, Michael
: APPLICANT: Roy, Natalie
: APPLICANT: Ikeda, John
: TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and
: Patent No. 6020127
: TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy
: FILE REFERENCE: 3477-112, 033477/139914
: CURRENT APPLICATION NUMBER: US/08/836,134A
: CURRENT FILING DATE: 1997-06-20
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 1232
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-08-836-134-2

Query Match      87.2% Score 6373.5; DB 3; Length 1232;
Best Local Similarity 95.9% Pred. No. 0;
Matches 1229; Conservative 1; Mismatches 1; Indels 51; Gaps 1;

OY 1 MATOQKASDERISQFDHNLPELSALIGDAVQLAKLEEEERAKKQKQNSQMRSE 60
|||||
DB 1 MATOQKASDERISQFDHNLPELSALIGDAVQLAKLEEEERAKKQKQNSQMRSE 60
|||||

OY 61 ARRLKTFVTEPYSSRITPOEMAAAGFTYGVNSGTCFCCSLILFGAGLTRLPIDHKRF 120
|||||
DB 61 ARRLKTFVTEPYSSRITPOEMAAAGFTYGVNSGTCFCCSLILFGAGLTRLPIDHKRF 120
|||||

OY 121 HPDCCGLLNKDVGNIAKYIRVKNLKSRLRGKRMROEERLASFRNMPFYVQGISPCV 180
|||||
DB 121 HPDCCGLLNKDVGNIAKYIRVKNLKSRLRGKRMROEERLASFRNMPFYVQGISPCV 180
|||||

OY 181 LSEAGFVFTGKODTVQCFSCGCLGNMBEGDDPMKEHAKWPKCEFLRSKSSSEITQYI 240
|||||
DB 181 LSEAGFVFTGKODTVQCFSCGCLGNMBEGDDPMKEHAKWPKCEFLRSKSSSEITQYI 240
|||||

OY 241 OSYKGFVDITGHEFVNSVQRELPMASAYCNDISFAYEELRLDSFKMDRESAVGYAALA 300
|||||
DB 241 OSYKGFVDITGHEFVNSVQRELPMASAYCNDISFAYEELRLDSFKMDRESAVGYAALA 300
|||||
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OY 301 KAGLEFYTGKIDIVOCFCGCGCLEKMOBGDPDLDDHTRCFPNCPFLONKSSAEVTPDIQS 360
DB 301 KAGLEFYTGKIDIVOCFCGCGCLEKMOBGDPDLDDHTRCFPNCPFLONKSSAEVTPDIQS 360
OY 361 RGEICELLETTSESNELEDSIAVGPVPEMAOGEAQMFOEAKNLNLOLAATTSASFRRMS 420
DB 361 RGEICELLETTSESNELEDSIAVGPVPEMAOGEAQMFOEAKNLNLOLAATTSASFRRMS 420
OY 421 LLDISSDLATDHLGCDLSIAASKHISKIPVOEPLVPEVFGNLNSVMCEBAGSGKTVLL 480
DB 421 LLDISSDLATDHLGCDLSIAASKHISKIPVOEPLVPEVFGNLNSVMCEBAGSGKTVLL 480
OY 481 KKIAPLMASSCCPLNRRPOLVFLVSLSTRPDEGLASIIDQOLEKESYTEMCNRIIO 540
DB 481 KKIAPLMASSCCPLNRRPOLVFLVSLSTRPDEGLASIIDQOLEKESYTEMCNRIIO 540
OY 541 QLNQOVFLDDYKEIGSIPOVIGKLOKNNLSRTCLLAVRTNRARDIRRYLETILEIQ 600
DB 541 QLNQOVFLDDYKEIGSIPOVIGKLOKNNLSRTCLLAVRTNRARDIRRYLETILEIQ 600
OY 601 APFFYNTVCILRLKLSHNMTRLRKRFMYFGKNOSLOKIOKTRPLVAAICAHMFOYPPDPS 660
DB 601 APFFYNTVCILRLKLSHNMTRLRKRFMYFGKNOSLOKIOKTRPLVAAICAHMFOYPPDPS 660
OY 661 FDDVAVERKSYMERLSLRNKATAEILKATVSSCGELALKGFFSCCFEENDDDLAAGVDED 720
DB 661 FDDVAVERKSYMERLSLRNKATAEILKATVSSCGELALKGFFSCCFEENDDDLAAGVDED 720
OY 721 EDLTMCLMSKFTNORLRPPRYRFLSPAFOEFLAGMRLLIELDSROEHOIDGLVHLKQINS 780
DB 721 EDLTMCLMSKFTNORLRPPRYRFLSPAFOEFLAGMRLLIELDSROEHOIDGLVHLKQINS 780
OY 781 PMMTYSAVNNFLNVYSSLPTKAGPKIYSHLLHLVDNKESELENISENDYDLKHOPEISIQ 840
DB 781 PMMTYSAVNNFLNVYSSLPTKAGPKIYSHLLHLVDNKESELENISENDYDLKHOPEISIQ 840
OY 841 MOLLGLMGOICPOAVFESVNSHELVLALKTAYOSNTVAACSPRYLOEIQGRITLIGALNT 900
DB 841 MOLLGLMGOICPOAVFESVNSHELVLALKTAYOSNTVAACSPRYLOEIQGRITLIGALNT 900
OY 901 QYFDPHRESLSLRSHIRPRGNKTSPPRAHFSYLETCGPKSOVPTIDODVSAFEPNEM 960
DB 901 QYFDPHRESLSLRSHIRPRGNKTSPPRAHFSYLETCGPKSOVPTIDODVSAFEPNEM 960
OY 961 ERNLAEKEDNVKSYMOMORASPOLSTGYKWLSPKQYKIPCLEVDVNDIDVGOQMLETL 1020
DB 961 ERNLAEKEDNVKSYMOMORASPOLSTGYKWLSPKQYKIPCLEVDVNDIDVGOQMLETL 1020
OY 1021 MTFVSAOSRIELHLNHSRGFIIESIRPALELSKASVTCISIKLELSAADELLTLPLSLE 1080
DB 1021 MTFVSAOSRIELHLNHSRGFIIESIRPALELSKASVTCISIKLELSAADELLTLPLSLE 1080
OY 1081 SLEVSQTTQSDODQIFPNLDKFLCKELSYDLGNINVFVSIPEEPFNHMEKLLIQISA 1140
DB 1081 SLEVSQTTQSDODQIFPNLDKFLCKELSYDLGNINVFVSIPEEPFNHMEKLLIQISA 1140
OY 1141 EYDSKLVKLVLIONSPNLHVHLKCNFSDGSLMTMLVCKKLTETIKRSDSFPQAVPVA 1200
DB 1141 EYDSKLVKLVLIONSPNLHVHLKCNFSDGSLMTMLVCKKLTETIKRSDSFPQAVPVA 1200
OY 1201 SLPRFISLKLINLEGOQFPDEETSEKFAVITIGLSNLEELLLPFGDGIYRAKLLIQOCC 1260
DB 1201 SLPRFISLKLINLEGOQFPDEETSEKFAVITIGLSNLEELLLPFGDGIYRAKLLIQOCC 1260
OY 1261 QLMHCLRVLSFFFTLNDSDVVEI 1282
DB 1261 QLMHCLRVLSFFFTLNDSDVVEI 1282
OY 1210 QLMHCLRVLSFFFTLNDSDVVEI 1231
DB 1210 QLMHCLRVLSFFFTLNDSDVVEI 1231

```

RESULT 2
 US-08-836-134-23
 : Sequence 23, Application US/08836134A
 : Patent No. 6020127

```

; GENERAL INFORMATION:
; APPLICANT: Mackenzie, Alex E.
; APPLICANT: Kornejuk, Robert G.
; APPLICANT: Mahadevan, Mani S.
; APPLICANT: McLean, Michael
; APPLICANT: Roy, Natalie
; TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and
; Patent No. 6020127
; FILE REFERENCE: Mutations Causing of Spinal Muscular Atrophy
; CURRENT APPLICATION NUMBER: US/08/836,134A
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 1151
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-836-134-23

```

Query Match 81.5%; Score 5955; DB 3; Length 1151;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1139; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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OY 1 MATOQASASERTISODPHNLPELSALGLDAVOLAKLEEEDEKERRAKMOGYNSOMRSE 60
DB 10 MATOQASASERTISODPHNLPELSALGLDAVOLAKLEEEDEKERRAKMOGYNSOMRSE 60
OY 61 ARKLFTVTEPYESSWIPQEMAAAGPYFTGVKSGICQFCCSILFLFGAGLTRPIDHNR 120
DB 70 ARKLFTVTEPYESSWIPQEMAAAGPYFTGVKSGICQFCCSILFLFGAGLTRPIDHNR 120
OY 121 HPDCGFLNKNVGNINAKYDTRVNLKSRRLGKMRQOESEARLASFRMPPYVOCISFCV 180
DB 130 HPDCGFLNKNVGNINAKYDTRVNLKSRRLGKMRQOESEARLASFRMPPYVOCISFCV 180
OY 181 LSENGFVTGKODTVOCFCGCGCLEKMOEGDDPMKEHAKMPKCEFLRSKSSSEITQYI 240
DB 190 LSENGFVTGKODTVOCFCGCGCLEKMOEGDDPMKEHAKMPKCEFLRSKSSSEITQYI 240
OY 241 QSKYGEVDITGEHFVNSVQRELPMASAYCNDISIFAYEBELRDSFKMPPRESAVCYAALA 300
DB 250 QSKYGEVDITGEHFVNSVQRELPMASAYCNDISIFAYEBELRDSFKMPPRESAVCYAALA 300
OY 301 KAGLEFYTGKIDIVOCFCGCGCLEKMOEGDDPLDDHTRCFPNCPFLONKSSAEVTPDIQS 360
DB 310 KAGLEFYTGKIDIVOCFCGCGCLEKMOEGDDPLDDHTRCFPNCPFLONKSSAEVTPDIQS 360
OY 361 RGEICELLETTSESNELEDSIAVGPVPEMAOGEAQMFOEAKNLNLOLAATTSASFRRMS 420
DB 370 RGEICELLETTSESNELEDSIAVGPVPEMAOGEAQMFOEAKNLNLOLAATTSASFRRMS 420
OY 421 LLDISSDLATDHLGCDLSIAASKHISKIPVOEPLVPEVFGNLNSVMCEBAGSGKTVLL 480
DB 430 LLDISSDLATDHLGCDLSIAASKHISKIPVOEPLVPEVFGNLNSVMCEBAGSGKTVLL 480
OY 481 KKIAPLMASSCCPLNRRPOLVFLVSLSTRPDEGLASIIDQOLEKESYTEMCNRIIO 540
DB 490 KKIAPLMASSCCPLNRRPOLVFLVSLSTRPDEGLASIIDQOLEKESYTEMCNRIIO 540
OY 541 QLNQOVFLDDYKEIGSIPOVIGKLOKNNLSRTCLLAVRTNRARDIRRYLETILEIQ 600
DB 550 QLNQOVFLDDYKEIGSIPOVIGKLOKNNLSRTCLLAVRTNRARDIRRYLETILEIQ 600
OY 601 APFFYNTVCILRLKLSHNMTRLRKRFMYFGKNOSLOKIOKTRPLVAAICAHMFOYPPDPS 660
DB 610 APFFYNTVCILRLKLSHNMTRLRKRFMYFGKNOSLOKIOKTRPLVAAICAHMFOYPPDPS 660
OY 661 FDDVAVERKSYMERLSLRNKATAEILKATVSSCGELALKGFFSCCFEENDDDLAAGVDED 720
DB 670 FDDVAVERKSYMERLSLRNKATAEILKATVSSCGELALKGFFSCCFEENDDDLAAGVDED 720

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QY 721 EDLTMCLSKFTAORLRFYRFLSPAFOEFLAGNRLIELLSDROEHODLGLYHLKQINS 780
Db 730 EDLTMCLSKFTAORLRFYRFLSPAFOEFLAGNRLIELLSDROEHODLGLYHLKQINS 789
QY 781 PMMTVSAYNNFLNYSVSLPSTRKACPKIVSHLLHLYDNKESLENISENDYKHKQPEISIQ 840
Db 790 PMMTVSAYNNFLNYSVSLPSTRKACPKIVSHLLHLYDNKESLENISENDYKHKQPEISIQ 849
QY 841 MOLLRLGLMOTICPOAFVSNSVSEHLVLAKTAYQSTNTVAACSPFYQLQGRITLIGALNTL 900
Db 850 MOLLRLGLMOTICPOAFVSNSVSEHLVLAKTAYQSTNTVAACSPFYQLQGRITLIGALNTL 909
QY 901 QYFDDHPEBSLILRSIHPIRGNKTSPPRAHFSVLETCFCDKSOVPTIIDDYASAFEPNEM 960
Db 910 QYFDDHPEBSLILRSIHPIRGNKTSPPRAHFSVLETCFCDKSOVPTIIDDYASAFEPNEM 969
QY 961 ERNLAEKEDNKSYMDQMRASPDLSGTGYMKSIPKQYKIPCLEVDVNDIDVVGQDMLEIL 1020
Db 970 ERNLAEKEDNKSYMDQMRASPDLSGTGYMKSIPKQYKIPCLEVDVNDIDVVGQDMLEIL 1029
QY 1021 MTVESASORIELHNSHGFIESTRPALELSKASTKCSISKLELSAEOELLTLPSLE 1080
Db 1030 MTVESASORIELHNSHGFIESTRPALELSKASTKCSISKLELSAEOELLTLPSLE 1089
QY 1081 SLEVSQTOSQDQIFPNLDKFLCKELSVDEGNINVSVPPEEPFNHHEKLLIOISA 1140
Db 1090 SLEVSQTOSQDQIFPNLDKFLCKELSVDEGNINVSVPPEEPFNHHEKLLIOISA 1149
QY 1141 E 1141
Db 1150 E 1150

RESULT 3
US-08-511-485-8
Sequence 8, Application US/08511485
Patent No. 5919912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
TITLE OF INVENTION: MAMMALIAN TAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
TYPE: amino acid

STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-8

Query Match 6.3%, Score 462; DB 2; Length 618;
Best Local Similarity 24.7%, Pred. No. 2,1e-33;
Matches 159; Conservative 93; Mismatches 238; Indels 154; Gaps 24;

QY 38 LEEBOKERAKOKGYNSOMRSEAKRLTFVTEPYSSMIP--OEMAAAGFTGVKSG 94
Db 28 LSDMTNSKOKKKYDFSC-----LYRMSYSTFPAGVPSERSLRAGYGVYNDK 80
QY 95 IOCCCSLLTGACGLTRLPEDHKRFHDDCGF--LKKDKGNIKYDIRKN----- 144
Db 81 VKFCGGLMDNMKLGDSPTIOKHOKLYPSCSTIONLVASASLASTSKNTPMKNISPAHSLS 140
QY 145 -----LKSRL-----RGCKMRY--OEEEARLASFRNMPFYVG 175
Db 141 PTLHSSILFSGYSYSLPPNPLNSRAVEDISSRTNPYAMSTEARFLTYHMP--LTF 198
QY 176 ISPCVLSAGVFTGKQDTVOGFCGCGGLGMNEEGDDPWKEHAKWPKCEFLRSKSSSE 235
Db 199 LSPSELARAGFYIIGPGRVACFACGKLSMNEPKDAMSEHRRHFPNCPFL--ENSE 255
QY 226 ITQYIOSKGFVDITGEHFVNSWVORELPMASATYNDISIFATEELRLDSFKDMPRESAVG 295
Db 256 TLRFSIS-----NLMOY-----HAARMKMTFYTWPPSSVPQ 286
QY 296 VAALKAGLFTYGIKDIYOCFSGCGCLERKQEGDDPLDDHPRCPNCPFIQNMKSSAEVT 355
Db 287 PQGLASAGFYVGRNDVYKCFGCGDGLRCWESGDDPWYEHAKWPKRCEFLIRMKQO-EFV 345
QY 356 PDLOGR-GEICELLETSESNEEDSIAGVPIYEMAGQPAQFOGAKNLEOLRAAYTSA 414
Db 346 DEIQGRYPHLEQLTSTSDTGTGEEN--ADPPIIHFGPESS--SEDAVMNPFVYSALEM 402
QY 415 SF-----RMSLDDISSD-----ANDHLGCGCLSTAS 442
Db 403 GNRDLVQVYLSKILTTGENTKYNDIVASALNEDEREKREKQAEKMSDLSLR 462
QY 443 KHISKPOEPLVLPVFNGL--NSVMCEVGEAGSGKTVL-----LKTAFIAMSQ----- 490
Db 463 KNRMLFQQLQCYLPILDLNLKANYINQEHDIQKQIPLQAEELIDTIWVKNMAAN 522
QY 491 ---CCPLNRQOLVYLSLSTR-----PDEGLASITCIDULEK--EGSYTEMCMNIT 539
Db 523 IFKNC---LKEIDSTLYKNLFDVKNMKYIPTEDVSGLSLEPOLRRIQERTRCKYCMDEKV 579
QY 540 QOLKQVLELDDYKEICSIPOVIGKLIOKNILSTCLLIIVRT 583
Db 580 ----SVVFIPCGHLVVC---QECAPSLKCPICIGITIGTVRT 615
RESULT 4
US-09-212-971-8
Sequence 8, Application US/092129718
Patent No. 6107041
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 60/017,354

us-09-830-338-1.ra1

APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF
TITLE OF INVENTION: IAPs AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATING
NUMBER OF INVENTION: 17
CORRESPONDENCE ADDRESSES: 17
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY:

Best Local Similarity	6.3%	Score	462	DB	3	Length	618
Matches	159	Conservative	24.7%	Pred.	No. 2.1e-33		

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: IBM Compatible

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-2000

APPLICATION NUMBER: 44-1996
FILING DATE: 60/017,354
TORYNEY/AGENT INFORMATION:
NAME: Rick

Michael Brady, Kristina
 REGISTRATION NUMBER:
 REFERENCE/DOCKET NUMBER: 07891/009001
 LECOMMUNICATION INFORMATION:
 TELEPHONE: 1

TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:

SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
TYPE: amino acids
TRANSDUCEDNESS: sfinal

ECULE TYPE: protein
0-929A-8

Match	6.38;	Score	462;	DB	4;	Length	618.
Local Similarity	24.78;	Pred	no				
150_2							

[illegible]

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LSQWINSNKKMKKYDSC-----LYRMSTYSTFPACVAVSEBSLARAGFYTYGVNDK 80
IQCFCCSLLEGAGLTRPLTEDHKRFRHPCGFG---LTKKDVGNTAKYDYNNK 80

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VKCFCCGLMDNWKIGDSPIQKHQOLYFSCSFIONLYSASLGSTSKNTSPMRNSFAHSLT 144
-----LKSP-----RGKMRY+CHPRA-----

PTLEHSSLFSGSYSSLPPNPLNSRAVEDISSRNTNPISYAMSTEARLTYIHMP--LTF 198
||| |
VEEARLASFRMPPFYVG

SPSELARAGFYIIGPGDRVACFACCGKLSNMPEPKDAMSEHRHIEPNCFLL---ENSLE 235
TOYIQSYKGFVDITGHEFNYSWYOFLPAAACAVR-----

[illegible][illegible]

*****1S5NEDSLAVGPVPEMAGEAOWFGEAKNLNEQLRAYTSA 414

Db 346 DEIGRYPHLEQLSTSDTGEEN--ADPPIHFGPESS--SEDAVAMNTPVYKSALEM 402
OY 415 SF-----RHMSLIDISDL-----ANDHLGCDLSTAS 442
Db 403 GFNDLVKQVLSKILTTGGENYKTVNDIVSALLNADEKREKEKQAEEMASDLSLIR 462
OY 443 KHISKPOEPLVLEVEFQNL---NSVMCEGEAGSGKTVL---LKKIAPILMASG----- 490
Db 463 KNRALFQQLTCLVPLIDNLKANKYINKQEHDIKQKQIPLQARELIDITWAGNAAN 522
OY 491 ---CCPLNRFQVLYLSLSTR-----PDEGLASIIDOLEK---EGSVTEMCMRNII 539
Db 523 IFKNC---LKEIDSTLYKNLFDVKNMKITYPEDVSGLSLEQLRLQGEERCKYCMQKEV 579
OY 540 QOLKNQVFLLDYKEICSPVOIGKLIQKNHLSRTCLLAVRT 583
Db 580 ---SVFIFPCGHLVVC---QECAPSLRKPCICRGITKTVRT 615

RESULT 6

US-08-569-749-2

Sequence 2, Application US/08569749

Patent No. 6187557

GENERAL INFORMATION:

APPLICANT: Rothe, Mike

TITLE OF INVENTION: INHIBITORS OF APOPTOSIS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESSES:

ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/569, 749

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Bieznert, David J.

REGISTRATION NUMBER: 24,774

REFERENCE/DOCKET NUMBER: A-62464/DJB

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415)781-1989

TELEFAX: (415)396-3249

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 618 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-569-749-2

Query Match 6.3%; Score 462; DB 4; Length 618;
Best Local Similarity 26.0%; Pred. NO. 2.1e-33;
Matches 155; Conservative 82; Mismatches 214; Indels 146; Gaps 22;

OY 38 LEEEOXKBRAMKQKGYNSOMSEAKRLKTFVYEPYSSWIP---OEMAAGFYFGVSG 94
Db 28 LSDWTNSKQKAKYFSC-----LYRMSTYTFPPAGVPSESLRAGGYTYGVNDK 80
OY 95 IOCFCCSILFLGAGLTRLPIDEDKRRHPDCGF---LANKDVGNIAKYDIRVN----- 144
Db 81 VKCFCCGMLMDWKLGSDPIQKHQOLYPSCSPIQNLVSAISGSGTSKNTSPMNSFAHSLS 140

OY 145 -----LKSRL-----RGKARY---QEEPARLASPRMPPVQ 175
Db 141 PTLHESSLPSCSYSSLSLSPNPLNSRAVEDISSRNPYSTAMSTERALTTHMP--ITF 198
OY 176 ISPCVLSBAGEVFTGKQDTVOCCFSCGGLGNWEEGDPMKEHAKWPCFELRSKSSSE 235
Db 199 LSPSELARAGFYTYIGRGVRVACFACGKLSNMPERDAMSHRRFRPCPL---ENBLE 255
OY 236 ITQYIQSYKGFVDITGEHFVNSWQRELPMASVCNDSIFAYEELRLDSFKOMPRESAVG 295
Db 256 TLFESIS-----NLSMQT-----HAARMFTFMYNPSVYVQ 286
OY 296 VAAALAKALFTYGIKDIYQCCSCGGLCKNQBEGDPLDDHTRCPNCFLOMKNSSAAYT 355
Db 287 PEQLASAFYVYVGRNDVCKCCDGLRCWESGDDPVWEHAKWPCFELIRMGO-EFV 345
OY 356 PDLQSR-GELELETTESNLEDSIAVPIYPERMAQEAQOFQAKMLNQLRAAYTSA 414
Db 346 DEIGRYPHLEQLSTSDTGEEN--ADPPIHFGPESS--SEDAVAMNTPVYKSALEM 402
OY 415 SFRHMSLIDISSDLATDHLGCDLSIAKSHISKVQEP-LVLEVEYNLSVMCEGEGAG 473
Db 403 GFNR-----DL-----VKQTVQSKILTTGGENYKTVNDIVSALLNAE 438
OY 474 SGKTVLLK-KIAFLMASGCCPLNRFQVLYLSLSTRPDEGLASIIDOLEKSGVTE 532
Db 439 DEKREEREKQAEEMASDLSLIRKRMALFQQLTCLVPL-----ILDNLK----- 484
OY 533 MCMRNIIQOLKNQVFLLDYKEICSPVOIGKLIQKNHLSRTCLLAVRTNRAADI 589
Db 485 ---ANVIKQEHDI-----KQKQIPLQARELID-----TIVKGNAAANI 523

RESULT 7

US-09-617-053A-8

Sequence 8, Application US/09617053A

Patent No. 6300492

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G

APPLICANT: Mackenzie, Alexander E

APPLICANT: Liston, Peter

APPLICANT: Baird, Stephen

APPLICANT: Tsang, Benjamin K

APPLICANT: Pratt, Christine

TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND

TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE

FILE REFERENCE: 07891/009003

CURRENT APPLICATION NUMBER: US/09/617, 053A

CURRENT FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 08/800, 929

PRIOR FILING DATE: 1997-02-13

NUMBER OF SEQ ID NOS: 17

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 8

LENGTH: 618

TYPE: PRT

ORGANISM: Homo sapiens

US-09-617-053A-8

Query Match 6.3%; Score 462; DB 4; Length 618;
Best Local Similarity 24.7%; Pred. NO. 2.1e-33;
Matches 159; Conservative 93; Mismatches 238; Indels 154; Gaps 24;

OY 38 LEEEOXKBRAMKQKGYNSOMSEAKRLKTFVYEPYSSWIP---OEMAAGFYFGVSG 94
Db 28 LSDWTNSKQKAKYFSC-----LYRMSTYTFPPAGVPSESLRAGGYTYGVNDK 80
OY 95 IOCFCCSILFLGAGLTRLPIDEDKRRHPDCGF---LANKDVGNIAKYDIRVN----- 144
Db 81 VKCFCCGMLMDWKLGSDPIQKHQOLYPSCSPIQNLVSAISGSGTSKNTSPMNSFAHSLS 140

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OY 145 -----LKSRL-----RGCKMRY--QEEEARLASFRNMPFYVQG 175
DB 141 PTLHSSLEFGSYSLSPNPLNSRAVEDISSRTNPNYSYAMSTEARFLTYHMP--LTF 198
OY 176 ISPCVLEAGFPFTGKOTVOCFCGCGCLGNMEGGDDPMKRAKMPKCEPLRSKSSSE 235
DB 199 LSPSLARAGFYIYIGPGDVACFCAGCGKLSNMEPKDAMSEHRHPPNCPFL--ENSLE 255
OY 236 ITOYIOSYKGFVDITGGEHFNVSWMQRELPMASAYCNDISFAYEELRDSFKDMPRESAVG 295
DB 256 TLRFSTIS-----NLSMOT-----HAARMRTFMWPSVVPYQ 286
OY 296 VAALAKAGLFYTGIDYVOCFCGCGCLEKMOEGDDPLDHTRCFPNCFLOMMSAEVT 355
DB 287 PEOLASAGFYVGRNDYKFCGCGCLRCWESGDDPMVHAHAKMPFRCFLRMKGQ--EFV 345
OY 356 PDLOS-R-GEICELLETTSSNLEDSIAVGPVPEMAOGEAOWFORAKNLNQLRAAYTSA 414
DB 346 DEIGCRPHLEQLSTSDTGTGEN--ADPPIIHFGPRESS--SEDAVMNTPPVYKSALEM 402
OY 415 SFRMSLSDISSDLATDHLGCDLSIAKHSKPYQEP-LVLPVEFGNLSVMCBEAG 473
DB 403 GFNRDLVKOTVLSKITLTGENTKYNDIVSALLNAEDEKREERKQAEEMASDLSLR 462
OY 443 KHISKPYQEPVLPVEFGNLT--NSVMCBEAGSGKTVL--LKKIPLAASG-----490
DB 463 KNRMALFOQLTCVPLIDNLKANVINKEHDIIKOKTOIPLQARLIDITIVKGNMAAN 522
OY 491 -----CCPLNRFQLVFYLSTSTR-----PDEGLASTICDOLLEK--EGSVTEMCMRNII 539
DB 523 IFKNC---LKEIDSTLTKNLFVDKNMKIYIPTEDEVSGLSLEEQRLQBERCKCMQMEYV 579
OY 540 QOLANOVFLFLDDYKEICSIPOVIGIKLQKNHLSRTCLLIARTNARDI 589
DB 580 -----SVFIPCGHLVYC---DECAPSLKRCPCICGIIKGYVRT 615

RESULT 8
US-09-069-023-29
: Sequence 29, Application US/09069023A
: Patent No. 6348573
: GENERAL INFORMATION:
: APPLICANT: Nunez, Gabriel
: APPLICANT: Inohara, Naohiro
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
: FILE REFERENCE: US-03333
: CURRENT APPLICATION NUMBER: US/09/069,023A
: NUMBER OF SEQ ID NOS: 38
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 29
: LENGTH: 618
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-069-023-29

```

```

Query Match 6.38; Score 462; DB 4; Length 618;
Best Local Similarity 26.08; Pct. No. 2.1e-33;
Matches 155; Conservative 82; Mismatches 214; Indels 146; Gaps 22;

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OY 38 LEEEOGKRAKOKGYSNOMSEAKRLKTEVTEPYSSWIP---QMAAAGFYTGVSNG 94
DB 28 LSDWYNMKNQMKKYDFSC-----LYRMSTYSTPPAGVYSESLARAGFYTGVDNK 80
OY 95 IQCFCCSLILFAGLITRPIEDHKRRHPDCGF---LNRDVGNIAKYDRIYVN-----144
DB 81 VKFCGCCGLMDNWKLSPTQKHKQLPSCSFQNLVNSASLSTSKNSPMRNSANLS 140
OY 145 -----LKSRL-----RGCKMRY--QEEEARLASFRNMPFYVQG 175

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DB 141 PTLHSSLEFGSYSLSPNPLNSRAVEDISSRTNPNYSYAMSTEARFLTYHMP--LTF 198
OY 176 ISPCVLEAGFPFTGKOTVOCFCGCGCLGNMEGGDDPMKRAKMPKCEPLRSKSSSE 235
DB 199 LSPSLARAGFYIYIGPGDVACFCAGCGKLSNMEPKDAMSEHRHPPNCPFL--ENSLE 255
OY 236 ITOYIOSYKGFVDITGGEHFNVSWMQRELPMASAYCNDISFAYEELRDSFKDMPRESAVG 295
DB 256 TLRFSTIS-----NLSMOT-----HAARMRTFMWPSVVPYQ 286
OY 296 VAALAKAGLFYTGIDYVOCFCGCGCLEKMOEGDDPLDHTRCFPNCFLOMMSAEVT 355
DB 287 PEOLASAGFYVGRNDYKFCGCGCLRCWESGDDPMVHAHAKMPFRCFLRMKGQ--EFV 345
OY 356 PDLOS-R-GEICELLETTSSNLEDSIAVGPVPEMAOGEAOWFORAKNLNQLRAAYTSA 414
DB 346 DEIGCRPHLEQLSTSDTGTGEN--ADPPIIHFGPRESS--SEDAVMNTPPVYKSALEM 402
OY 415 SFRMSLSDISSDLATDHLGCDLSIAKHSKPYQEP-LVLPVEFGNLSVMCBEAG 473
DB 403 GFNR-----DL-----VKOTVOSKITLTGENTKYNDIVSALLNAE 438
OY 474 SGRTVLK-KIAPLASGCCPLNRFQLVFYLSTSTRPDEGLASTICDOLLEKESVTE 532
DB 439 DEKREERKQAEEMASDLSLRNRMALFOQLTCVLP-----LDMNLK-----484
OY 533 MCMRNIOQLKNOVFLFLDDYKEICSIPOVIGIKLQKNHLSRTCLLIARTNARDI 589
DB 485 -----ANVINKEHDII-----KOKTOIPLQARLID-----TIVKGNMAANI 523

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RESULT 9
PCT-US96-12860-2
: Sequence 2, Application PC/TUS9612860
: GENERAL INFORMATION:
: APPLICANT: TULARIK, INC.
: TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSER: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US96/12860
: FILING DATE: 06 AUG 1996
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Brezner, David J.
: REGISTRATION NUMBER: 24,774
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415)781-1989
: TELEFAX: (415)398-3249
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 618 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
PCT-US96-12860-2

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COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: Pasteo for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/800,929A

FILING DATE: 13-FEB-1997

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/030,590

FILING DATE: 14-NOV-1996

APPLICATION NUMBER: 60/017,354

FILING DATE: 26-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Bleker-Brady, Kristina

REGISTRATION NUMBER:

REFERENCE/DOCKET NUMBER: 07891/009001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-428-0200

TELEFAX: 617-428-7045

TELEX:

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 612 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-800-929A-14

Query Match
 Best Local Similarity 26.68; Score 457.5; DB 4; Length 612;
 Matches 148; Conservative 73; Mismatches 207; Indels 129; Gaps 19;

QY 43 OKERAKMKG---YNSOMRSEAK-----RLKTFVTEPYSSWIP--QEMAAGFYET 89
 DB 16 OKLRIMKSTILSNMTKESEKMFDFSCGLYRMSTYSAPFRGVPVSESLARAGFYET 75
 QY 90 GYKSGICFCGCSLLIFGAGLRLPIEDHKRFHPDCGF--LANKDVGNLAXYDRIYKLNK 146
 DB 76 GYNDKVKFCGGLMDNMKGDSPEVKHROFYPCSFVOTLLSASLOSPK--NMSPVK 132
 QY 147 SRL-----RGG-----KMYQEERLASFRRMPFYVQ 174
 DB 133 SRFAHSSPLERGGIHSNLCSSPLNSRAVEDSSRMDCSYAMSTEERARLTYSMWP--LS 190
 QY 175 GISPCVLSAEGFVFTGKODTYOCFSCGCCGLNWEBCDDPKKHAHAKWPKCEFLRSKSS 234
 DB 191 FLSPAELARAGFYIGPDRVACFACGCKLSMWERKDDAMSEHRRHFPHPCELENTSETQ 250
 QY 235 EITQYIQSYKGFVDITGEHFNVSWMQRELPMASAYCNDISFAVEELRLDSFKDMPRESAV 294
 DB 251 RFS-----ISNLSMOTHSARLRTFLYWPSPV 278
 QY 295 GVAALAKAGLFYTGINDYOCFSCGCCGLNWEBCDDPKKHAHAKWPKCEFLRSKSSAEV 354
 DB 279 QPQLASAGFYIYVNRDVKFCFCGGLRCMHPGDDPWIEHAKWPKCEFLIRMKGO--EF 337
 QY 355 TPDLOS--GELCELLETSESUNLEDSIAGVPIVEMAGQAGWFOEAKNLNQLRAAYIS 413
 DB 338 VDEIQARYPHLEQLSTSDTPGEBNADPTETVYHFGPGB-----SS 379
 QY 414 ASFRHMSLLDSSDLATDHLIGCDLSIASKISKPYQEPVLVPEVGNUNSVWCV---E 469
 DB 380 KDVMWSTPPVYKALE---NGFSRLYROTVOQL---LATGENTRTVNDIVSYVLNAE 432
 QY 470 GEAGSGKTVLLKTAFLMASGCCPLNRLQOLVYVYLSLSTRPDEGLASITCOLLEKSGS 529
 DB 433 DERREEEK---ENQTEPMASGDSLIRKNNMALFOQLTHVLP-----LIDNLL--EAS 480
 QY 530 VTENCMNITIOQLKNQV 546

DB 481 VITKQEHDIRO-KTQI 496

RESULT 12

US-08-569-749-14

Sequence 14, Application US/08569749

Patent No. 6187557

GENERAL INFORMATION:

APPLICANT: Rothe, Mike

TITLE OF INVENTION: INHIBITORS OF APOPTOSIS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/569,749

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Brezner, David J.

REGISTRATION NUMBER: 24,774

REFERENCE/DOCKET NUMBER: A-62464/DJB

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415)398-3249

TELEFAX: (415)398-3249

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 612 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-569-749-14

Query Match
 Best Local Similarity 26.68; Score 457.5; DB 4; Length 612;
 Matches 148; Conservative 73; Mismatches 207; Indels 129; Gaps 19;

QY 43 OKERAKMKG---YNSOMRSEAK-----RLKTFVTEPYSSWIP--QEMAAGFYET 89
 DB 16 OKLRIMKSTILSNMTKESEKMFDFSCGLYRMSTYSAPFRGVPVSESLARAGFYET 75
 QY 90 GYKSGICFCGCSLLIFGAGLRLPIEDHKRFHPDCGF--LANKDVGNLAXYDRIYKLNK 146
 DB 76 GYNDKVKFCGGLMDNMKGDSPEVKHROFYPCSFVOTLLSASLOSPK--NMSPVK 132
 QY 147 SRL-----RGG-----KMYQEERLASFRRMPFYVQ 174
 DB 133 SRFAHSSPLERGGIHSNLCSSPLNSRAVEDSSRMDCSYAMSTEERARLTYSMWP--LS 190
 QY 175 GISPCVLSAEGFVFTGKODTYOCFSCGCCGLNWEBCDDPKKHAHAKWPKCEFLRSKSS 234
 DB 191 FLSPAELARAGFYIGPDRVACFACGCKLSMWERKDDAMSEHRRHFPHPCELENTSETQ 250
 QY 235 EITQYIQSYKGFVDITGEHFNVSWMQRELPMASAYCNDISFAVEELRLDSFKDMPRESAV 294
 DB 251 RFS-----ISNLSMOTHSARLRTFLYWPSPV 278
 QY 295 GVAALAKAGLFYTGINDYOCFSCGCCGLNWEBCDDPKKHAHAKWPKCEFLRSKSSAEV 354
 DB 279 QPQLASAGFYIYVNRDVKFCFCGGLRCMHPGDDPWIEHAKWPKCEFLIRMKGO--EF 337


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OY 355 TPOLQSR-GEICELLETTSSENEEDS:IAVGRIYEMAGQOMFOEAKNNEDQRAAYTS 413
Db 338 VDEIOAKRPILLEULLSTSDTPGEEMADPTIETVYHFGPGE-----SS 37/9
OY 414 ASFRMSLIDISSDLATDHLGCDLSIAHSKISKPVOEPLVLEPEFGNLNSVVCY----E 469
Db 380 EDVVMSSPPVYKALE---MGFSRLVRQYQNOI---LATGENTYVADIVSYLLNAE 432
OY 470 GEAGSGKTVLLKTAFTLMASGCCPLNRFQVLVYLSSTRPDEGLASTICDOLLEKEGS 529
Db 433 DEREEEEK---EROTEEMASGDSLIRKRNMALEFOQLTHVLP-----ILDNLL--EAS 480
OY 530 VTEMCMRNIIQOLKNV 546
Db 481 VITROEHDIRQ-KTQI 496

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RESULT 13
US-09-617-053A-14
Sequence 14: Application US/09617053A
Patent No. 6300492
GENERAL INFORMATION:
APPLICANT: Korneluz, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
TITLE OF INVENTION: NADP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US/08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 612
TYPE: PRT
ORGANISM: Mus musculus
US-09-617-053A-14

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Query Match	6.38	Score	457.5	DB 4	Length	612
Best Local Similarity	26.68	Pred. No.	5.3e-33			
Matches 148; Conservative	73	Mismatches	207		Indels	129
					Gaps	19

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OY 43 OKERKKQKGG---NNSQRRSEAK-----RLKTFVYIEPSSMIP---QEMAAAGCYET 89
Db 16 OKIKRIMKSTILSNMTRKSESEKKKPPSCSLCYHMSYTSAPRQVPSSESLNAGCYTT 75
OY 90 GYKSGIOCFCCSLLIFGAGLTRLEIDHKRRHPCCGF---LKNQVGNIAKYDIRVANK 146
Db 76 GYNDKVKCFCEGGLMDNMKQGDSPVEKHROPYPCSFVQITLLSLQSPSK---NMSPVK 132
OY 147 SRL-----RGC-----KMYQDEARLASFRNMPYVQ 174
Db 133 SRFAHSPLEBGGHISNLCSPLNSRAVEDPSSRMDPCSYAMSTEARPLTYSMP-LS 190
OY 175 GISPVLSAEPVFTGKODTYQCSGCGCLGNMBEGDDPKMEHAKKNTPKCEFLRSKSSSE 234
Db 191 FLSPSELARAFYYIIGEDRACACCGKLSNMPEKPDAMSEHNRHPHPCFLENTSETQ 250
OY 235 EITQYIQSYKGFVDITGEHFVNSVQRELPMAASAYCNDISLFEIILDSFKDMPRESAV 294
Db 251 RFS-----ISLMSQTHSARLRLFLYMPPEVP 278
OY 295 GVALAKAGLGYTGIKDIVQCFSGCGGLEKKQOEGDDPLDHTKCFPMCFPLQNMKSSAEV 354
Db 279 QPEOLASGFIYVVRNDYKCFCCDDGGLRCWPEPDDPIEIAKKFPRCEFLIRNKGQ-EP 337

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[illegible]

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Query Match	6.3%	Score	457.5	DB	5	Length	612
Best Local Similarity	26.6%	Pred. NO.	5.3e-33				
Matches	148	Conservative	73	Mismatches	207	Indels	129
						Gaps	19

Qy 43 OERKKNKMG-----YNSQRSEAK-----RLKTFVTEYEPSSIP---QDMAAGCYFT 89
Db 16 OXLRKIMKSTILSWTKMESEKMKFDPSCELRYMSTYSAPRCVYSEBSLACGFYTT 75
Qy 90 GYKSGIOCFCSLLIFGAGLRPLRPEDHKRRHPDQGF---LNLKDVGNIAATYDIRVKNLK 144
Db 76 GYNDVCKEFCFGGLMIDNNKQSGPVEKIRHOPYPSGCSFYQTLKSLSDSPK---NMSBPV 133

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QY 147 SRL-----RG-----KRYOEERARLAFRAMPFYVO 174
Db 133 SRFHSSPLERGGIHSNLCSSPLNSNAVEDFSSRMDPCSYAMSTEARFLTYSMP--LS 190
QY 175 GISCVSEAGFVFTGKODTVOCFSCGCGCLGNWEGDDPKREHAKWPCFELRSKSSSE 234
Db 191 FLSPAEIARAGFYIIGPGRVACFACGKLSNWEPRKDAEMSEHRHFPCHCPLLENTSETQ 250
QY 235 EITQYIOSYKGFVDITGEHFVNSWQRELPMASACNCSITAYEELRLDSFKDMPRESAV 294
Db 251 RFS-----ISNLSMOTHSARLRTFLYPPSPV 278
QY 295 GVALAKAGLFTYGIKDIYOCSCGCGCLEKQOEGDDPLDHTRCFPNCPFLONKSSAEV 354
Db 279 OPEOLASAGFYIYDNDKRCFCDCGGLRCWEPDDEPRHAKWPCFELRLKKG-EP 337
QY 355 TPDLOS-GEICELLETTSESNEIETSIAGPIVPEMAGEQWFOEAKNLEOLRAAYS 413
Db 338 VDEIARVPHLEQLLSTSDTPGEMNDPTEYVHFGPGE-----SS 379
QY 414 ASFRHMSLDDISDLATDHLGCDLSIASKHSKPVQEPVLPEVFGNLSVMCV-----E 469
Db 380 EDVYMSRTPVYKALE---MGFSRLVROTVOROI---LATGENTRYNDIVSYLNAE 432
QY 470 GEAGSGVLLKTAFLMASGCCPLNRFOLVFLYLSSTRDEGLASTICCOLLEKESG 529
Db 433 DERREER---EROTEMASGDLIRKKNMALFOQLHVLP-----ILDNL--BAS 480
QY 530 VTEMCMNIIQOLKNOV 546
Db 481 VITQOEHDIIRQ-KTOI 496

RESULT 15
US-09-212-971-12
; Sequence 12, Application US/09212971B
; Patient No. 6107041
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009002
; CURRENT APPLICATION NUMBER: US/09/212,971B
; EARLIER FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 60/017,354
; EARLIER FILING DATE: 1996-04-26
; EARLIER APPLICATION NUMBER: 60/030,590
; EARLIER FILING DATE: 1996-11-14
; EARLIER APPLICATION NUMBER: 08/800,929
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-212-971-12

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Query Match
Best Local Similarity 6.0%; Score 440; DB 3; Length 600;
Matches 145; Conservative 88; Mismatches 226; Indels 162; Gaps 19;

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QY 47 AKMKGYS-----QMRSEARKLTFTVTEYSSWIP---QEMAAAGFYFTGVKSGIOCF 98
Db 9 AKIMKSADTFELKDFSCGLYRLS---TYSAPRGVPSERSISLIRAGFYTTGANDKVKCF 65

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QY 99 CCLILFAGAGLRLPIEDKRRHPDCCGLLNKDVGNIAKYDIRVKNLSRLRGKMY-- 156
Db 66 CCGILMDNKKQODSPMEHRRKLYPCNMFVOTLNPANSLEASPRSLSTANSTMPUSFAS 125
QY 157 -----OEEERLASFRNMPFYVOGIS 177
Db 126 SENTGYFSGSYSSFPDSEVNFNANDCPALSTSPYHFRAMNTEARLITYETWP--LSFLS 183
QY 178 PCVLSEAGFVFTGKODTVOCFSCGCGCLGNWEGDDPKREHAKWPCFELRSKSSSEIT 237
Db 184 PAKLAKAGFYIIGDGRACACGKLSNWEPRKDAEMSEHQRHFPSCFPLKDLGOS----- 239
QY 238 QIYSKGFVDITGEHFVNSWQRELPMASAYCNDST-FAYEELRLDSFKDMPRESAVCV 296
Db 240 -----ASRYVSNLSMOTHSARLRTFSSNPPSSALVHS 271
QY 297 AALAKAGLFTYGIKDIYOCSCGCGCLEKQOEGDDPLDHTRCFPNCPFLONKSSAEVTP 356
Db 272 QELASAGFYITGHSDDYKCCDCGGLRCWESGDDPWVEHAKWPCFELRLKKG-EP 331
QY 357 DIOSRGELCELLETTSESNEIETSIAGPIV-----PMAGEQWFOEA 400
Db 332 VOAGYPHLEQLLSTSDSP-EDENADAIYHFGPESSEDDVYMSRTPVYKALEMGFSRS 390
QY 401 ---KNLEQDRAA---YTSASFRHMSLDDISDL-----ATHLLGCDLSIASKHSK 447
Db 391 LVROTVOROIATGENTRYVSDVIGLIDABDEMREQEMQAAEEESDDIALIRKNKY 450
QY 448 PVQE-PLVPEVFGNLSVMCVGEAGSGKTVLLKTAFLMASGCCPLNRFOLVFLYLSL 506
Db 451 LFOHLTCVTPMLYCLLSARAITEQECNAV----- 480
QY 507 SSTRPDEGLASTICDOLLEKESVTEMCMNIIQOLKNOV---LFLLDYK-----EICS 558
Db 481 --QKPHTLQASTLIDTVLAK-GNTAATSFRNSLEIDPALYRIDIFVQODIRSLPTDIAA 537
QY 559 IP--OVICKLLOKHNLSYTC 577
Db 538 LPMEQLRLK-LQERRMCKVC 557

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Search completed: September 30, 2002, 15:04:59
Job time: 245 sec